

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 22:28:25 ; Search time 5208.63 Seconds  
(without alignments)  
16556.656 Million cell updates/sec

Title: US-09-852-209A-2

Perfect score: 2108

Sequence: 1 cccgcgcgtgagtgctct.....nctttttgaaataataaa 2108

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_ov.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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5	1979.4	93.9	2849	6	AX391260	AX391260 Sequence
6	1979.4	93.9	2849	6	AX464152	AX464152 Sequence
7	1979.4	93.9	3007	6	AX234498	AX234498 Sequence
8	1979.4	93.9	3007	9	AF091434	AF091434 Homo sapi
9	1625.6	77.1	1804	6	AF739931	AF739931 Sequence
10	1625.6	77.1	1804	9	AF260738	AF260738 Homo sapi
11	1624.8	77.1	1760	6	AR267280	AR267280 Sequence
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15	1465.2	59.5	1817	9	AB033831	AB033831 Homo sapi
16	1261.6	59.8	1328	6	BD004757	BD004757 Novel VEG
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18	1030.2	48.9	196952	9	AC093608	AC093608 Homo sapi
19	1030.2	48.9	196952	9	AC093608	AC093608 Homo sapi
20	994.8	47.2	1095	6	AX027935	AX027935 Sequence
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22	959.4	45.5	3571	10	AF266467	AF266467 Mus muscu
23	959.4	45.5	3571	6	AR267281	AR267281 Sequence
24	959.4	45.5	3571	6	AR282985	AR282985 Sequence
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27	957.8	45.4	2692	10	AF117608	AF117608 Mus muscu
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31	734.4	34.8	1035	6	AR282950	AR282950 Sequence
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36	331.8	15.7	82113	2	AC015451	AC015451 Homo sapi
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38	287	13.6	300	6	AX027962	AX027962 Sequence
39	287	13.6	300	6	AX027981	AX027981 Sequence
40	284	13.5	284	6	AX027963	AX027963 Sequence
41	284	13.5	284	6	AX027982	AX027982 Sequence
42	283.4	13.4	289	6	AX027970	AX027970 Sequence
43	283.4	13.4	289	6	AX027993	AX027993 Sequence
44	279	13.2	279	6	AX027968	AX027968 Sequence
45	279	13.2	279	6	AX027989	AX027989 Sequence

# ALIGNMENTS

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DEFINITION Homo sapiens platelet-derived growth factor C mRNA, complete cds.  
ACCESSION AF244813  
VERSION AF244813.1 GI:8866883  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2152)  
Li,X., Ponten,A., Aase,K., Karlsson,L., Abramson,A., Utela,M.,  
Backstrom,G., Hellstrom,M., Bostrom,H., Li,H., Soriano,P.,  
Betscholtz,C., Heidin,C.-H., Alitalo,K., Ostman,A. and Eriksson,U.

Pred. No. is the number of results predicted by chance to have a

TITLE PDGF-C is a new protease-activated ligand for the PDGF  
 JOURNAL alpha-receptor  
 MEDLINE Nat. Cell Biol. 2 (5), 302-309 (2000)  
 PUBMED 20268201  
 REFERENCE 2 (bases 1 to 2152)  
 AUTHORS Eriksson, U., Aase, K., Li, X. and Ponten, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-MAR-2000) Ludwig Institute for Cancer Research,  
 Nobels vag 3 P.O. Box 240, Stockholm S-171 77, Sweden  
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 /tissue\_type="lung"  
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 CDCVCGSGTG" 621 a 424 c 476 g 630 t 1 others

CDS

BASE COUNT 621 a 424 c 476 g 630 t 1 others  
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Query Match 94.9%; Score 1999.6; DB 9; Length 2152;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Qy 61 GTGACATCTGCCCTTGGCGGCGGAGACGAGCGGAGCTCAGCGGGAATCCAACTGAGTAGT 120  
 Db 213 GTGACATCTGCCCTTGGCGGCGGAGACGAGCGGAGCTCAGCGGGAATCCAACTGAGTAGT 272  
 Qy 121 AATATCCAGTTCCTGACACACGAGGACGAGCGGAGTACAGATCCTCAGCATGAGAGA 180  
 Db 273 AATATCCAGTTCCTGACACACGAGGACGAGCGGAGTACAGATCCTCAGCATGAGAGA 332  
 Qy 181 ATTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
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 Db 453 ACCTTTGATGAAGATTTGGGCTTTGAAGACCCAGAGATGACATATGCAAGTATGATTTT 512  
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1981 CTGGACAAAATATACATGTA 2000
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RESULT 2
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DEFINITION Sequence 1 from patent US 6391311.
ACCESSION AR210624
VERSION AR210624.1 GI:21513401
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 2825)
  Ferrara, N. and Kuo, S.S.
  Polypeptides having homology to vascular endothelial cell growth
  factor and bone morphogenetic protein 1
  Patent: US 6391311-A 1 21-May-2002;
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Best Local Similarity 97.7%; Pred. No. 0;
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Db 344 AATTCCAGTTTTCAGCAACAGAGAACAGAGTACAGATCTCTCAGCATGAGAGAA 403
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REFERENCE 1  
 AUTHORS Ferraraz, N., Williams, P.M., Baker, K.P., Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L., Kuo, S.S., Mark, M.R., Marsters, S.A., Pitti, R.M., Wood, W.I., Gerber, H., Gerritsen, M.E., Paoni, N.F. and Watanabe, C.K.  
 TITLE Promotion or inhibition of angiogenesis and cardiovascularization  
 JOURNAL Patent: WO 0073445-A 3 07-DEC-2000;  
 Genentech Inc. (US)

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AX464152

LOCUS

DEFINITION

ACCESSION

AX464152

Sequence 285 from Patent WO0140466.

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PAT 16-JUL-2002

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VERSION AX464152.1 GI:21899092
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SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.O., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L., and Zhang, Z.
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DEFINITION Sequence 32 from patent US 6495668.  
ACCESSION AR267280  
VERSION AR267280.1 GI:29697283  
KEYWORDS Unknown.

ORGANISM	Unknown.	Unclassified.
REFERENCE	1 (bases 1 to 1760)	
AUTHORS	Gilbert, T., Hart, C.E., Sheppard, P.O. and Gilbertson, D.G.	
TITLE	Growth factor homolog ZVEGF4	
JOURNAL	Patent: US 6495668-A 32 17-DEC-2002;	
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Best Local Similarity	99.7%; Pred. No. 0;	
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BASE COUNT 494 a 373 c 411 g 482 t

ORIGIN

Query Match 77.1%; Score 1624.8; DB 6; Length 1760;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1637; Conservative 1; Mismatches 3; Indels 1; Gaps 1;  
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RESULT 15

AB033831

LOCUS

DEFINITION

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AB033831

AB033831.1

spinal cord-derived growth factor; scd3f gene.

KEYWORDS

spinal cord-derived growth factor; scd3f gene.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AB033831 1817 bp mRNA linear PRI 26-JUL-2000  
Homo sapiens hscd3f mRNA for spinal cord-derived growth factor.



Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (sites)  
Hamada,T., Ui-Tei,K. and Miyata,Y.  
A novel gene derived from developing spinal cords, SCDGF, is a  
unique member of the PDGF/VEGF family  
FEBS Lett. 475 (2), 97-102 (2000)  
20317014  
10858496  
2 (bases 1 to 1817)  
Hamada,T., Ui-Tei,K. and Miyata,Y.  
Direct Submission  
Submitted (25-OCT-1999) Tsuyoshi Hamada, Nippon Medical School,  
Department of Pharmacology, 1-1-5, Sendagi, Bunkyo-ku, Tokyo  
113-8602, Japan (E-mail:t-hamada@nms.ac.jp,  
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Wed Nov 26 13:03:28 2003

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Search completed: November 26, 2003, 03:42:33  
Job time : 5217.63 secs



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 PR 21-MAY-1999; 99US-0135426.  
 PR 15-JUN-1999; 99US-0144022.  
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 PA (UYHE-) UNIV HELSINKI LICENSING LTD.  
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 PI Oestman A, Heldin C, Betscholz C;  
 XX WPI; 2000-292954/25.  
 DR P-PSDB; AAY84557.  
 XX Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,  
 PT differentiation, growth and motility of cells expressing the PDGF-C  
 PT receptor -  
 XX Claim 9; Fig 1; 135pp; English.  
 PS The present sequence encodes human platelet-derived growth factor C  
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 CC ability to stimulate and enhance proliferation or differentiation,  
 CC and/or growth or motility of cells expressing a PDGF-C receptor.  
 CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell  
 CC proliferation, preferably in combination with one other growth factor  
 CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also  
 CC be used for stimulating connective tissue or wound healing. The  
 CC PDGF-C polypeptide can be enzymatically processed to generate the active  
 CC truncated form of PDGF-C and used to regulate the receptor-binding  
 CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast  
 CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.  
 CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour  
 CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.  
 CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma  
 CC and erythroleukemia, can be identified by testing for expression of  
 CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue  
 CC remodelling during invasion of tumour cells into a normal population of  
 CC cells. Antagonists can also be used to treat fibrotic conditions,  
 CC especially found in the lung, kidney or liver.  
 XX  
 SQ Sequence 2108 BP; 623 A; 400 C; 451 G; 629 T; 5 other;

Query Match 99.8%; Score 2103.6; DB 21; Length 2108;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGCCGTGAGTGAGCTCTACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTG 60  
 DB 1 CCCGCCGTGAGTGAGCTCTACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTG 60  
 QY 61 GTGACATCTGCCCTGGCCGGCCAGAGACGAGGACTCAGGGCGAATCCAACTGAGTAGT 120  
 DB 61 GTGACATCTGCCCTGGCCGGCCAGAGACGAGGACTCAGGGCGAATCCAACTGAGTAGT 120  
 QY 121 AAATTCAGTTTTCAGCAACAGAGAACAGACGAGTACAGATCCCTCAGCATGAGAGA 180  
 DB 121 AAATTCAGTTTTCAGCAACAGAGAACAGACGAGTACAGATCCCTCAGCATGAGAGA 180  
 QY 181 ATTATTACTGTCTACTAAATGGAAGTATTACAGCCCAAGGTTTCCTCATCTTATCCA 240  
 DB 181 ATTATTACTGTCTACTAAATGGAAGTATTACAGCCCAAGGTTTCCTCATCTTATCCA 240  
 QY 241 AGAATAACGGTCTTGATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACCT 300  
 DB 241 AGAATAACGGTCTTGATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACCT 300  
 QY 301 AGTTTGTATGAAGATTTGGGCTTCAGACCCAGAGATGACATATGCAAGTATGATTT 360  
 DB 301 AGTTTGTATGAAGATTTGGGCTTCAGACCCAGAGATGACATATGCAAGTATGATTT 360  
 QY 361 GTAGAAGTGTAGGAACCCAGTCATGGAACATATATTAGGCGCTGTGTGGTTCTCGTACT 420  
 DB 361 GTAGAAGTGTAGGAACCCAGTCATGGAACATATATTAGGCGCTGTGTGGTTCTCGTACT 420

Db 361 GTAGAAGTGTAGGAACCCAGTCATGGAACATATATTAGGCGCTGTGTGGTTCTCGTACT 420  
 QY 421 GTACAGGAAAACAGATTTCTAAAGGAATCAAATTAGGATAAGATTTGTATCTCATGAA 480  
 Db 421 GTACAGGAAAACAGATTTCTAAAGGAATCAAATTAGGATAAGATTTGTATCTCATGAA 480  
 QY 481 TATTTTCTCTCTGAACCAAGGTTCTGCATCCACTACAACATTTGTCTCATGCAATTCACA 540  
 Db 481 TATTTTCTCTCTGAACCAAGGTTCTGCATCCACTACAACATTTGTCTCATGCAATTCACA 540  
 QY 541 GAAGCTGTGAGTCTTCTAGTCTACCCCTTTCAGCTTTGGCCACTGGACTGCTTAAATAT 600  
 Db 541 GAAGCTGTGAGTCTTCTAGTCTACCCCTTTCAGCTTTGGCCACTGGACTGCTTAAATAT 600  
 QY 601 GCTATAACTGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTTGAACAGAGATGG 660  
 Db 601 GCTATAACTGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTTGAACAGAGATGG 660  
 QY 661 CAGTTGGACTTTAGAGATCTATATAGGCCAACTTTGGCAACTTTCTTGGCAAGGCTTTTGT 720  
 Db 661 CAGTTGGACTTTAGAGATCTATATAGGCCAACTTTGGCAACTTTCTTGGCAAGGCTTTTGT 720  
 QY 721 TTTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAAACAGAGAGGTAAAGATTATAC 780  
 Db 721 TTTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAAACAGAGAGGTAAAGATTATAC 780  
 QY 781 AGCTGCACACCTCGTAACCTTCTCAGTGTCCATAGGGGAAGAACTAAAGAGAACCGATACC 840  
 Db 781 AGCTGCACACCTCGTAACCTTCTCAGTGTCCATAGGGGAAGAACTAAAGAGAACCGATACC 840  
 QY 841 ATTTTCTGGCAGGTTGTCTCTCTGTTAAACGCTGTGTGGGAACTGTGCTGTGTTCTC 900  
 Db 841 ATTTTCTGGCAGGTTGTCTCTCTGTTAAACGCTGTGTGGGAACTGTGCTGTGTTCTC 900  
 QY 901 CACAAATTCGAATGATGTCCTCAATGTCCTCAACAGCAAGTACTTAAATAATACCAACGAGTC 960  
 Db 901 CACAAATTCGAATGATGTCCTCAATGTCCTCAACAGCAAGTACTTAAATAATACCAACGAGTC 960  
 QY 961 CTTCAAGTTGAGACCAAGAACCCGGTGTCAAGGGGATTCGCAAAATCACTCACCCAGCTGGCC 1020  
 Db 961 CTTCAAGTTGAGACCAAGAACCCGGTGTCAAGGGGATTCGCAAAATCACTCACCCAGCTGGCC 1020  
 QY 1021 CTGAGACACCATAGGAGTGTGACTGTGTGTCAGAGGAGACACAGGAGGATAGCCGAT 1080  
 Db 1021 CTGAGACACCATAGGAGTGTGACTGTGTGTCAGAGGAGACACAGGAGGATAGCCGAT 1080  
 QY 1081 CACCAACAGCAGCTCTTCCAGAGCTGTGAGTGTGAGTGGCTGATTTATTAGAGAACG 1140  
 Db 1081 CACCAACAGCAGCTCTTCCAGAGCTGTGAGTGTGAGTGGCTGATTTATTAGAGAACG 1140  
 QY 1141 TATCGTTTATCTCCATCTTAATCTCAGTTGTTTCTTCAAGGACCTTTTCATCTTCAGGA 1200  
 Db 1141 TATCGTTTATCTCCATCTTAATCTCAGTTGTTTCTTCAAGGACCTTTTCATCTTCAGGA 1200  
 QY 1201 TTTACAGTGCATTTCTGAAAAGAGAGACATCAAAAGAAATAGGAGTGTGTGAAACAGCTCT 1260  
 Db 1201 TTTACAGTGCATTTCTGAAAAGAGAGACATCAAAAGAAATAGGAGTGTGTGAAACAGCTCT 1260  
 QY 1261 TTTGAGAGGAGGCTTAAAGGACAGAGAAAAGGCTCTCAATCGTGGAAAGAAAATTAAT 1320  
 Db 1261 TTTGAGAGGAGGCTTAAAGGACAGAGAAAAGGCTCTCAATCGTGGAAAGAAAATTAAT 1320  
 QY 1321 GTTGTATTAAATAGATCAACAGCTAGTTTTCAGAGTTACCATGTACGTATTCACCTAGCTG 1380  
 Db 1321 GTTGTATTAAATAGATCAACAGCTAGTTTTCAGAGTTACCATGTACGTATTCACCTAGCTG 1380  
 QY 1381 GGTCTGTATTTCAGTCTTTCGATACCGCTTAGGTTAATGTGCTAGTACAGAAAATAACT 1440  
 Db 1381 GGTCTGTATTTCAGTCTTTCGATACCGCTTAGGTTAATGTGCTAGTACAGAAAATAACT 1440  
 QY 1441 GTGCAAGTGAGCAGCTGATTCGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1500  
 Db 1441 GTGCAAGTGAGCAGCTGATTCGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1500



Db 524 CGTTTGATGAAGATTGGCTTGAAGACCAGAGATGATCATATGCAAGTATGATTTTG 583  
QY 362 TAGAAGTTGAGAACCCAGATGAGAACTATATTTAGGGCGCTGCTGGTCTTCTGGTACTG 421  
Db 584 TAGAAGTTGAGAACCCAGATGAGAACTATATTTAGGGCGCTGCTGGTCTTCTGGTACTG 643  
QY 422 TACCAGGAAACAGATTCTTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATGAAT 481  
Db 644 TACCAGGAAACAGATTCTTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATGAAT 703  
QY 482 ATTTTCTCTTGAACAGGGTTCTGATCCACTACAACTTGTATGCGCCCAAAATTCACAG 541  
Db 704 ATTTTCTCTTGAACAGGGTTCTGATCCACTACAACTTGTATGCGCCCAAAATTCACAG 763  
QY 542 AAGCTGTGAGTCTCTCAGTCTACCCCTTTCAGCTTTGGCCACTGGACCTGCTTAAATAATG 601  
Db 764 AAGCTGTGAGTCTCTCAGTCTACCCCTTTCAGCTTTGGCCACTGGACCTGCTTAAATAATG 823  
QY 602 CTATTAACCTGCTTTAGTACCTTGGAAAGACCTTATTCGATATCTTGAAACCAAGAGATGGC 661  
Db 824 CTATTAACCTGCTTTAGTACCTTGGAAAGACCTTATTCGATATCTTGAAACCAAGAGATGGC 883  
QY 662 AGTTGGACTTAGAGATCTATATAGGCCAACTTTGGCAACTTCTTGGCAAGGCTTTTGTGT 721  
Db 884 AGTTGGACTTAGAGATCTATATAGGCCAACTTTGGCAACTTCTTGGCAAGGCTTTTGTGT 943  
QY 722 TTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAAGAGAGGTAAAGATTATACA 781  
Db 944 TTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAAGAGAGGTAAAGATTATACA 1003  
QY 782 GCTGCAACCTCGTAATCTTCAAGTTCCTAATAGGGAAGAACTAAAGAGAACCGATACCA 841  
Db 1004 GCTGCAACCTCGTAATCTTCAAGTTCCTAATAGGGAAGAACTAAAGAGAACCGATACCA 1063  
QY 842 TTTTCTGGCCAGGTTGTCTCTGTTAAACGCTGTGGTGGAACTGTGCTGTGCTCTCC 901  
Db 1064 TTTTCTGGCCAGGTTGTCTCTGTTAAACGCTGTGGTGGAACTGTGCTGTGCTCTCC 1123  
QY 902 ACAATTGCAATGTAATGTGTCCCAAGCAAAAGTTACTAAAAATACCAAGAGTCC 961  
Db 1124 ACAATTGCAATGTAATGTGTCCCAAGCAAAAGTTACTAAAAATACCAAGAGTCC 1183  
QY 962 TTCAGTTGAGACCAAGACCGGTGTGAGGGATTTGCAAAATCACTACCGAGTGGCCC 1021  
Db 1184 TTCAGTTGAGACCAAGACCGGTGTGAGGGATTTGCAAAATCACTACCGAGTGGCCC 1243  
QY 1022 TGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGATACCGCATC 1081  
Db 1244 TGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGATACCGCATC 1303  
QY 1082 ACCACAGAGCTCTTTGCCAGAGCTGTGAGTGTGAGTGTGCTGATTTCTATTAGAGAACGT 1141  
Db 1304 ACCACAGAGCTCTTTGCCAGAGCTGTGAGTGTGAGTGTGCTGATTTCTATTAGAGAACGT 1363  
QY 1142 ATGCGTTATCTCATCTCTAACTCTCAGTTGTTTTCCTCAGGACCTTCTATCTTCAGGAT 1201  
Db 1364 ATGCGTTATCTCATCTCTAACTCTCAGTTGTTTTCCTCAGGACCTTCTATCTTCAGGAT 1423  
QY 1202 TTACAGTGCATTCTGAAAGAGGAGACATCAAAAGAAATTAGGAGTTGTGCAACAGCTCTT 1261  
Db 1424 TTACAGTGCATTCTGAAAGAGGAGACATCAAAAGAAATTAGGAGTTGTGCAACAGCTCTT 1483  
QY 1262 TTGAGAGGAGGCTTAAAGACAGGAGAAAGGTCCTCAATCGTGGAAAGAAATTAATG 1321  
Db 1484 TTGAGAGGAGGCTTAAAGACAGGAGAAAGGTCCTCAATCGTGGAAAGAAATTAATG 1543  
QY 1322 TTGTATTAATAGATCACAGCTAGTTTTCAGAGTTACCATGTACGTAATCCACTAGCTGG 1381  
Db 1544 TTGTATTAATAGATCACAGCTAGTTTTCAGAGTTACCATGTACGTAATCCACTAGCTGG 1603  
QY 1382 GTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTGATGACAGGAAAAAATG 1441  
Db 1604 GTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTGATGACAGGAAAAAATG 1663

QY 1442 TGCAAGTGAACCTGATTCGCTTGCCTTAACTCTAAAGCTCCATGTCTGGGCT 1501  
Db 1664 TGCAAGTGAACCTGATTCGCTTGCCTTAACTCTAAAGCTCCATGTCTGGGCT 1723  
QY 1502 AAAATCGTATAAATCTGGATTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAAC 1561  
Db 1724 AAAATCGTATAAATCTGGATTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAAC 1783  
QY 1562 AGAACATTTCTATGTACTACAACTGGTTTTTAAAAAGGAACCTATGTTGCTATGAATTA 1621  
Db 1784 AGAACATTTCTATGTACTACAACTGGTTTTTAAAAAGGAACCTATGTTGCTATGAATTA 1843  
QY 1622 ACTTGTGCTGTGTATAGGACAGCTGGATTTTTTCTATTTCTTATTTAAAAATTTCTGCC 1681  
Db 1844 ACTTGTGCTGTGTATAGGACAGCTGGATTTTTTCTATTTCTTATTTAAAAATTTCTGCC 1903  
QY 1682 ATTTAGAAGAGAGAACTACATTTTCATGTTTGAAGAGATAAACTCTGAAAGAGAGTGG 1741  
Db 1904 ATTTAGAAGAGAGAACTACATTTTCATGTTTGAAGAGATAAACTCTGAAAGAGAGTGG 1963  
QY 1742 CCTTATCTTCACCTTTATCGATAAGTCAGTTTATTTGTTTCATTTGTGTGTACATTTTATAT 1801  
Db 1964 CCTTATCTTCACCTTTATCGATAAGTCAGTTTATTTGTTTCATTTGTGTGTACATTTTATAT 2023  
QY 1802 CTCCTTTTGCATTTAACTGTTTGGCTTTTCTAACTCTTGTAAATATATCTATTTTATACC 1861  
Db 2024 CTCCTTTTGCATTTAACTGTTTGGCTTTTCTAACTCTTGTAAATATATCTATTTTATACC 2083  
QY 1862 AAAGGTATTTAAATTTCTTTTATGACAACTTAGATCAACTATTTTACCTTTGGTAAAT 1921  
Db 2084 AAAGGTATTTAAATTTCTTTTATGACAACTTAGATCAACTATTTTACCTTTGGTAAAT 2143  
QY 1922 TTTTCTAAACACAAATTTTATAGCCAGAGAGCAAAAGATGATATAAAATATTTGTGCC 1981  
Db 2144 TTTTCTAAACACAAATTTTATAGCCAGAGAGCAAAAGATG--ATATAAAATATTTGTTC 2200  
QY 1982 CTGACAAAAATACATGTATNTCCATCCCGGAATGTTCTAGAGTTGGATTAAACCTGCA 2041  
Db 2201 TCTGACAAAAATACATGTATTTT-CATCTCGTATGTTGCTAGAGTTAGATT-AATCTGCA 2258  
QY 2042 TTTTAAAAAACCTGAAATTTGGGAANGAANTGTAAGTTGGCCAAANCTTTTTTGAAAA 2101  
Db 2259 TTTTAAAAAACCTGAAATTT--GGAATAGAATTTGTAAGTT--GCAAAAGACTTTTTTGAAAA 2312  
QY 2102 TAATTA 2108  
Db 2313 TAATTA 2319

## RESULT 3

ABS57294

ID ABS57294 standard; DNA; 2825 BP.

XX ABS57294;

AC ABS57294;

XX ABS57294;

DT 31-JAN-2003 (first entry)

XX DNA encoding human vascular endothelial cell growth factor-E (VEGF-E).

DE Human; vascular endothelial cell growth factor-E; VEGF-E; PRO:200;

XX VEGF; bone morphogenetic protein 1; wound repair; tissue regeneration;

KW cardiovascular disorder; endothelial disorder; angiogenic disorder;

KW cancer; diabetes mellitus; cardiac hypertrophy; atherosclerosis;

KW cardiant; cytostatic; antidiabetic; antiarteriosclerotic;

KW gene therapy; gene; ds.

XX Homo sapiens.

OS Homo sapiens.

XX Key

FH Location/Qualifiers

FT 259..1296

FT /\*tag= a

FT /product= "VEGF-E"

FT

XX	US6455283-B1.
PN	
XX	
PD	24-SEP-2002.
XX	
PX	10-MAR-1999; 99US-0265686.
PF	
PR	17-MAR-1998; 98US-0040220.
PR	02-NOV-1998; 98US-0184216.
XX	(GETH ) GENENTECH INC.
PA	
XX	Ferrara N, Kuo SS;
PI	
XX	
DR	WPI; 2003-066231/06.
DR	P-PSDB; ABG72132.
XX	
PT	New nucleic acid encoding endothelial cell growth factor-E polypeptide,
PT	useful for diagnosing or treating a cardiovascular, endothelial or
PT	angiogenic disorder such as cancer, diabetes mellitus or
PT	atherosclerosis -
XX	
FS	Claim 2; Fig 1; 46pp; English.
XX	
CC	The present invention relates to the isolation of human vascular
CC	endothelial cell growth factor-E (VEGF-E, also referred to as
CC	PRO:200), and the polynucleotide sequence encoding it. VEGF-E is
CC	related to VEGF and bone morphogenetic protein 1. VEGF-E is useful
CC	in wound repair, as well as in the generation and regeneration of
CC	tissue. The sequences of the invention are useful for diagnosing or
CC	treating cardiovascular, endothelial or angiogenic disorders such as
CC	cancer, diabetes mellitus, cardiac hypertrophy and atherosclerosis.
CC	The polynucleotide encoding VEGF-E is useful in the gene therapy of
CC	such disorders. The present sequence encodes human VEGF-E.
XX	
SQ	Sequence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;
Query Match 93.9%; Score 1979.4; DB 25; Length 2825;	
Best Local Similarity 97.7%; Pred. No. 0;	
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;	
QY	2 CCGCCGTGAGTGAGCTTCAACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCCTCGTG 61
Dd	224 CCGCCGTGAGTGAGCTTCAACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCCTCGC 283
QY	62 TGACATCTGCCCTGGCGGCAGACAGCGGACTCAGGCGGAATCAAACCTGAGTAGTA 121
Dd	284 TGACATCTGCCCTGGCGGCAGACAGCGGACTCAGGCGGAATCCAACCTGAGTAGTA 343
QY	122 AAATTCCAGTTTTCCAGCAAACAAGGAACAAGCGAGTACAAGATCCCTCAGCATGAGAGA 181
Dd	344 AAATTCCAGTTTTCCAGCAAACAAGGAACAAGCGAGTACAAGATCCCTCAGCATGAGAGA 403
QY	182 TTATTACTGTGTTCTAATAATGGAAGTATTCACAGCCCCAAGGTTTCCTCATCTTATCCAA 241
Dd	404 TTATTACTGTGTTCTAATAATGGAAGTATTCACAGCCCCAAGGTTTCCTCATCTTATCCAA 463
QY	242 GAATAACGGCTTGGTATGAGATTAGTACAGTAGAGGAATAATGTATGATACAACTTA 301
Dd	464 GAATAACGGCTTGGTATGAGATTAGTACAGTAGAGGAATAATGTATGATACAACTTA 523
QY	302 CGTTTGATGAAGATTTGGGCTTGAAGACCAGAAGATGACATATGCAAGTATGATTTTG 361
Dd	524 CGTTTGATGAAGATTTGGGCTTGAAGACCAGAAGATGACATATGCAAGTATGATTTTG 583
QY	362 TAGAAGTTGAGGAACCCAGTGATGGAACATATATTAGGGCCCTCGTGTTCTTGSTACTG 421
Dd	584 TAGAAGTTGAGGAACCCAGTGATGGAACATATATTAGGGCCCTCGTGTTCTTGSTACTG 643
QY	422 TACCAGGAAAACAGATTTCTTAAGGAATCAAATTAGGATAAGATTGTATCTGATGAAT 481
Dd	644 TACCAGGAAAACAGATTTCTTAAGGAATCAAATTAGGATAAGATTGTATCTGATGAAT 703

Db	1784	AGAA	CAITCTA	GTACTACAA	ACTGGTTTTTAA	AGGA	CTA	GTGCTAT	GAATTA	1843	
Qy	1622	ACTT	GTGTCRT	GCTGATAG	CAGACATG	GAATTTTTC	TATATCT	TATTA	AAAAATTTCT	GC	1681
Db	1844	ACTT	GTGTCAT	GCTGATAG	CAGACATG	GAATTTTTC	TATATCT	TATTA	AAAAATTTCT	GC	1903
Qy	1682	ATTT	TAGAAG	AGAGACTAC	ATTCAT	TGTTGGA	AGAGATAA	AACTG	AAAGAGAGTGG	1741	
Db	1904	ATTT	TAGAAG	AGAGAACTAC	ATTCAT	TGTTGGA	AGAGATAA	AACTG	AAAGAGAGTGG	1963	
Qy	1742	CTT	TATCTT	CACTTTAT	CGATAAGT	CAGTTTAT	TGTTCT	CACTG	TACATTTTTAT	T	1801
Db	1964	CTT	TATCTT	CACTTTA	CGATAAGT	CAGTTTAT	TGTTCT	CACTG	TACATTTTTAT	T	2023
Qy	1802	CTC	CTTTG	CAATTA	TAACCTG	TGGCTTTTCT	TAATCT	TGTTT	AAATATATCT	TATTTTACC	1861
Db	2024	CTC	CTTTT	TGCAATTA	TAACTG	TGGCTTTTCT	TAATCT	TGTTT	AAATATATCT	TATTTTACC	2083
Qy	1862	AAAG	TAATTA	ATCTCTTT	TATGAC	CACTT	TAGTCA	CACTATTT	TAGCTTGGTAA	T	1921
Db	2084	AAAG	TAATTA	ATCTCTTT	TATGAC	CACTT	TAGTCA	CACTATTT	TAGCTTGGTAA	T	2143
Qy	1922	TTTT	CTAA	CAATTTG	TATAG	CCAGAG	CAAAAGAT	GATGATA	AAAAATAT	TGTTGCC	1981
Db	2144	TTTT	CTAA	CACAATTTG	TATAG	CCAGAG	CAAAAGATG	---	ATATAA	TATTTGTTGC	2200
Qy	1982	CTG	CAAAAA	TACATG	TATNTCC	ATCCG	GAATGGT	GCTAG	AGTTGGAT	TAAACCTGCA	2041
Db	2201	TCT	GACAAAA	TACATG	TATTT-CA	TCTCG	TATGGT	GCTAG	AGTTAGAT	T- AATCTGCA	2258
Qy	2042	TTTT	TAAAA	AACTCG	AAATTTGG	GAANG	GAATTTGG	TATGG	CTGGCC	AAANCCTTTTGGAAA	2101
Db	2259	TTTT	TAAAA	AACTG	AATTT- - -	GGAAT	TAGATTTGG	TAAAGTT- - -	GCAAA	GACTTTTGGAAA	2312
Qy	2102	TAAT	TA	2108							
Db	2313	TAAT	TA	2319							

[illegible]



QY 542 AGCTGTGAGTCTTCAGTGTCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATATG 601  
Db 793 AAGCTGTGAGTCTTCAGTGTCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATATG 852  
QY 602 CTATTAAGTCTTACCTTGGAGAGCTTATTCGATATCTTGAACAGAGAGATGGC 661  
Db 853 CTATAAGTCTTACCTTGGAGAGCTTATTCGATATCTTGAACAGAGAGATGGC 912  
QY 662 AGTTGAGCTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTGGCAAGCTTTTGT 721  
Db 913 AGTTGAGCTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTGGCAAGCTTTTGT 772  
QY 722 TTGGAGAGAAATCCAGAGTGTGATCTGAACCTTAAACAGAGAGATGAATATACA 781  
Db 973 TTGGAGAGAAATCCAGAGTGTGATCTGAACCTTAAACAGAGAGATGAATATACA 1032  
QY 782 GCTGCACACCTCGTAATCTTCAGTGTCCATAGGGAAGAACTTAAGAGAACCGATACA 841  
Db 1033 GCTGCACACCTCGTAATCTTCAGTGTCCATAGGGAAGAACTTAAGAGAACCGATACA 1092  
QY 842 TTTTCTGGCCAGGTTCTCTCGTGTAAAGCTGTGGTGGAACTGTGCTGTGCTCC 901  
Db 1093 TTTTCTGGCCAGGTTCTCTCGTGTAAAGCTGTGGTGGAACTGTGCTGTGCTCC 1152  
QY 902 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTTACTAAATAATACCAGAGTCC 961  
Db 1153 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTTACTAAATAATACCAGAGTCC 1212  
QY 962 TTCAGTTGAGACCAAGACCGGTGTCCAGGGATTCACAAATCACTCACGAGGTGGCC 1021  
Db 1213 TTCAGTTGAGACCAAGACCGGTGTCCAGGGATTCACAAATCACTCACGAGGTGGCC 1272  
QY 1022 TGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGAGGACACAGAGGATAGCCGCATC 1081  
Db 1273 TGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGAGGACACAGAGGATAGCCGCATC 1332  
QY 1082 ACCACAGAGCTCTTCCAGAGCTGTGCAGTGTGAGTGTGCTATATAGAGAACGT 1141  
Db 1333 ACCACAGAGCTCTTCCAGAGCTGTGCAGTGTGAGTGTGCTATATAGAGAACGT 1392  
QY 1142 ATCGTTATCTCCATCTTAATCTCAGTGTCTTTCAGGACCTTTCATCTTCAGGAT 1201  
Db 1393 ATCGTTATCTCCATCTTAATCTCAGTGTCTTTCAGGACCTTTCATCTTCAGGAT 1452  
QY 1202 TTACAGTGTCAATCTGAAAGAGGAGACATCAAAAGAAATAGGAGTTGTGCAACAGCTCT 1261  
Db 1453 TTACAGTGTCAATCTGAAAGAGGAGACATCAAAAGAAATAGGAGTTGTGCAACAGCTCT 1512  
QY 1262 TTGAGAGGCGCTTAAGAGGACAGAGAAAGGTCTTCAATCGTGGAAAGAAATTAATG 1321  
Db 1513 TTGAGAGGCGCTTAAGAGGACAGAGAAAGGTCTTCAATCGTGGAAAGAAATTAATG 1572  
QY 1322 TTGTATTAAATAGATCACACAGCTAGTTTTCAGAGTTACCAATGATTCACATAGCTG 1381  
Db 1573 TTGTATTAAATAGATCACACAGCTAGTTTTCAGAGTTACCAATGATTCACATAGCTG 1632  
QY 1382 GTTCTGTATTTCAGTCTTTCGATAGCGCTTACGCTTACGCTACAGGAAAGAACTG 1441  
Db 1633 GTTCTGTATTTCAGTCTTTCGATAGCGCTTACGCTTACGCTACAGGAAAGAACTG 1692  
QY 1442 TGCAAGTGAGCACCTGATTCGGTTCCTTAACTCTTAAAGCTCCATGCTCCGGCCCT 1501  
Db 1693 TGCAAGTGAGCACCTGATTCGGTTCCTTAACTCTTAAAGCTCCATGCTCCGGCCCT 1752  
QY 1502 AAAATCGTATAAATCTGGATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1561  
Db 1753 AAAATCGTATAAATCTGGATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1812  
QY 1562 AGAATCTTATGTACTACAACTGGTCTTTTAAAGAGAACTATGTTGCTATGAATTA 1621  
Db 1813 AGAATCTTATGTACTACAACTGGTCTTTTAAAGAGAACTATGTTGCTATGAATTA 1872  
QY 1622 ACTTGTGTCTGTGATAGGACAGCTGGATTTTCTTATTTTCTTATTAATTTCTGCC 1681

Db 1873 ACTTGTGTCTGTGATAGGACAGCTGGATTTTCTATATTTCTTATTAATTTCTGCC 1932  
QY 1682 ATTTAGAGAGAGAACTATCATTCATCGTGTGGAGAGATAAACCTGAAAAGAGAGTGG 1741  
Db 1933 ATTTAGAGAGAGAACTATCATTCATCGTGTGGAGAGATAAACCTGAAAAGAGAGTGG 1992  
QY 1742 CCTTATCTTCACTTTATCGATAAGTCACTTATTTGTTTTCATTCGTGTACATTTTATTT 1801  
Db 1993 CCTTATCTTCACTTTATCGATAAGTCACTTATTTGTTTTCATTCGTGTACATTTTATTT 2052  
QY 1802 CTCTTTTGAACATTAATCACTTGTGGCTTTTCTAATCTTGTGTAAATATATCTATTTTACC 1861  
Db 2053 CTCTTTTGAACATTAATCACTTGTGGCTTTTCTAATCTTGTGTAAATATATCTATTTTACC 2112  
QY 1862 AAAGGTATTTAATATCTTTTATGACAACTTAGTCACTATTTTGTAGCTTGTGTAAT 1921  
Db 2113 AAAGGTATTTAATATCTTTTATGACAACTTAGTCACTATTTTGTAGCTTGTGTAAT 2172  
QY 1922 TTTTCTAAACAACTTGTATAGCCAGAGGAAACAAAGATGATATAAAATATTTTGTGCC 1981  
Db 2173 TTTTCTAAACAACTTGTATAGCCAGAGGAAACAAAGATG---ATATAAATATTTGTGC 2229  
QY 1982 CTGGACAAAAATACATGATATNTCCATCCCGAATGGTGTAGAGTTGGATTAACCTGCA 2041  
Db 2230 TCTGACAAAAATACATGATATTT-CATTCTCGTATGGTGTAGAGTTAGATT-AAATCTGCA 2287  
QY 2042 TTTTAAAAAACTCGAATTTGGGAANGAANTTTGTAAGTTGGCCAAACNTTTTGTGAAA 2101  
Db 2288 TTTTAAAAAACTGAATTT---GGAATAGATTTGGTAAGTT---GCAAGAGACTTTTGTGAAA 2341  
QY 2102 TAATTA 2108  
Db 2342 TAATTA 2348  
RESULT 5  
AAZ34296  
ID AAZ34296 standard; cDNA; 2849 BP.  
XX AC AAZ34296;  
XX AC AAZ34296;  
DT 07-DEC-1999 (first entry)  
XX Human PRO200 nucleotide sequence.  
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein; ss.  
XX Homo sapiens.  
XX WO9946281-A2.  
XX 16-SEP-1999.  
XX 08-MAR-1999; 99WO-US05028.  
XX 10-MAR-1999; 98US-0077450.  
PR 11-MAR-1999; 98US-0077632.  
PR 11-MAR-1999; 98US-0077641.  
PR 11-MAR-1999; 98US-0077649.  
PR 12-MAR-1999; 98US-0077791.  
PR 13-MAR-1999; 98US-0078004.  
PR 17-MAR-1999; 98US-0040220.  
PR 20-MAR-1999; 98US-0078886.  
PR 20-MAR-1999; 98US-0078910.  
PR 20-MAR-1999; 98US-0078936.  
PR 20-MAR-1999; 98US-0078939.  
PR 25-MAR-1999; 98US-0079294.  
PR 26-MAR-1999; 98US-0079656.  
PR 27-MAR-1999; 98US-0079663.  
PR 27-MAR-1999; 98US-0079664.

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PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.

XX (GETH ) GENENTECH INC.
XX PA
XX PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI; 1999-551358/46.
XX P-PSDB; AAY41766.
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders -
XX Claim 2; Fig 206; 530pp; English.
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as
XX sources of probes, primers, for chromosome mapping, and for generation
XX of antisense sequences. They can also be used to create transgenic
XX animals. The proteins can be used to treat a variety of diseases and
XX disorders, depending on their function. Diseases that may be treated
XX include blood coagulation disorders, cancers and cellular adhesion
XX disorders. They may also be used to raise antibodies. AA23891 to
XX AA23438, and AAY41685 to AAY41774 represent polynucleotide and
XX polypeptide sequence given in the exemplification of the present
XX invention.
XX SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 93.9%; Score 1979.4; DB 20; Length 2849;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCCGCCGTGAGTGAGCTCTCACCCAGTCAGCCCAATGAGCTCTTCGGGCTTCCTCGG 61
DB 250 CCCGCCGTGAGTGAGCTCTCACCCAGTCAGCCCAATGAGCTCTTCGGGCTTCCTCGG 309
QY 62 TGACATCTGCCCTGGCCGCCAGAGCAGGAGGACTCAGCGGAATCCCACTCAGTAGTA 121
DB 310 TGACATCTGCCCTGGCCGCCAGAGCAGGAGGACTCAGCGGAATCCCACTCAGTAGTA 369
QY 122 AATCCAGTTTCCAGCAACAAGGAACAGAACGGAGTCAAGATCCTCAGCATGAGAGAA 181
DB 370 AATCCAGTTTCCAGCAACAAGGAACAGAACGGAGTCAAGATCCTCAGCATGAGAGAA 429
QY 182 TTATTACTGTGTCTACTAATGGAAGTATTCAGAGTCAAGGTTCTCTCATCTATCCAA 241
DB 430 TTATTACTGTGTCTACTAATGGAAGTATTCAGAGTCAAGGTTCTCTCATCTATCCAA 489
QY 242 GAAATACGGTCTTGATGAGATTAGTAGCAGTAGAGGAAATGTATGATACAACTTA 301
DB 490 GAAATACGGTCTTGATGAGATTAGTAGCAGTAGAGGAAATGTATGATACAACTTA 549
QY 302 CGTTTGATGAAGATTTCGGCTTGAGACCCGAGAGATGACATATGCAAGTATGATTTTG 361
DB 550 CGTTTGATGAAGATTTCGGCTTGAGACCCGAGAGATGACATATGCAAGTATGATTTTG 609
QY 362 TAGAAGTTGAGAACCCAGTGTATGAACTATATTAGGCGCTGCTGCTGCTGCTGCTG 421
DB 610 TAGAAGTTGAGAACCCAGTGTATGAACTATATTAGGCGCTGCTGCTGCTGCTGCTG 669
QY 422 TACCAGGAAAACAGATTTCTAAAGGAAATCAAAATTTAGGATAGATTTGTATCTGATGAAT 481
DB 670 TACCAGGAAAACAGATTTCTAAAGGAAATCAAAATTTAGGATAGATTTGTATCTGATGAAT 729
QY 482 ATTTTCCTTCTGAACCCAGGTTCTGCATCCACTACAAATTTGTCATGCAATTCACAG 541
DB 730 ATTTTCCTTCTGAACCCAGGTTCTGCATCCACTACAAATTTGTCATGCAATTCACAG 789
QY 542 AAGCTGTGAGTCCCTTCAGTGTCTACCCCTTCAGCTTTCAGCTTTCAGCTTTCAGT 601
DB 790 AAGCTGTGAGTCCCTTCAGTGTCTACCCCTTCAGCTTTCAGCTTTCAGCTTTCAGT 849
QY 602 CTATAACTGCCTTTAGTAGTACCTTGAAGAGACCTTATTTCGATATCTTTGAACAGAGATGCC 661
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Db 850 CTATAACTGCGCTTTAGTACCTTGAAGACCTTATTCGATATCTTTGAACCCAGAGAGATGCG 909  
 Qy 662 AGTTGGACCTTGAAGATCTATATAGGCCAACTTGGCAACTCTTTGGCAAGCGCTTTTGT 721  
 Db 910 AGTTGGACCTTGAAGATCTATATAGGCCAACTTGGCAACTCTTTGGCAAGCGCTTTTGT 969  
 Qy 722 TTGGAAGAAATCCAGAGTGTGATCTGAACCTTCTAACAGAGAGGTGAAGATTATACA 781  
 Db 970 TTGGAAGAAATCCAGAGTGTGATCTGAACCTTCTAACAGAGAGGTGAAGATTATACA 1029  
 Qy 782 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA 841  
 Db 1030 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA 1089  
 Qy 842 TTTTCTGCGCAGGTGTCTCTCGTTTAAACGCTGTGTGGGAACTGTGCTGTGTCTCC 901  
 Db 1090 TTTTCTGCGCAGGTGTCTCTCGTTTAAACGCTGTGTGGGAACTGTGCTGTGTCTCC 1149  
 Qy 902 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTTAAAAAATACCAAGAGTCC 961  
 Db 1150 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTTAAAAAATACCAAGAGTCC 1209  
 Qy 962 TTCAGTTGAGACCAAGACCGGTGTCAAGGATTCACAAATCACTCAACGAGTGGCCC 1021  
 Db 1210 TTCAGTTGAGACCAAGACCGGTGTCAAGGATTCACAAATCACTCAACGAGTGGCCC 1269  
 Qy 1022 TGGAGCACCATGAGGAGTGTCACTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGATC 1081  
 Db 1270 TGGAGCACCATGAGGAGTGTCACTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGATC 1329  
 Qy 1082 ACCACGACGAGCTTTGCCAGAGCTGTGCAAGTGTGAGTGTGCAAGAGTGTGCAAGAGTGT 1141  
 Db 1330 ACCACGACGAGCTTTGCCAGAGCTGTGCAAGTGTGAGTGTGCAAGAGTGTGCAAGAGTGT 1389  
 Qy 1142 ATGGTTATCTCCATCTTAATCTCAGTGTGTGCTTCAAGGACCTTTCATCTTCAGAT 1201  
 Db 1390 ATGGTTATCTCCATCTTAATCTCAGTGTGTGCTTCAAGGACCTTTCATCTTCAGAT 1449  
 Qy 1202 TTACAGTGCATCTTGAAGAGAGAGACATCAACAGATTTAGGAGTGTGCAAGAGTGT 1261  
 Db 1450 TTACAGTGCATCTTGAAGAGAGAGACATCAACAGATTTAGGAGTGTGCAAGAGTGT 1509  
 Qy 1262 TTGAGAGAGGCGCTTAAAGGACAGAGAAAGGCTTCAATCGTGGAAAGAAATTAATG 1321  
 Db 1510 TTGAGAGAGGCGCTTAAAGGACAGAGAAAGGCTTCAATCGTGGAAAGAAATTAATG 1569  
 Qy 1322 TTGTTATTAATAGATCACAGCTAGTTTTCAGAGTTTACCATGTAGCTATTCACCTAGCTGG 1381  
 Db 1570 TTGTTATTAATAGATCACAGCTAGTTTTCAGAGTTTACCATGTAGCTATTCACCTAGCTGG 1629  
 Qy 1382 GTTCTGTATTTTCAGTCTTTTCGATACGGCTTAGGGTAATGTCAAGTACAGGAAAAAATG 1441  
 Db 1630 GTTCTGTATTTTCAGTCTTTTCGATACGGCTTAGGGTAATGTCAAGTACAGGAAAAAATG 1689  
 Qy 1442 TGCAAGTACAGACCTGATTCGTTGCTTCAATCTTAAGCTTCAATGTCCCTGGGCT 1501  
 Db 1690 TGCAAGTACAGACCTGATTCGTTGCTTCAATCTTAAGCTTCAATGTCCCTGGGCT 1749  
 Qy 1502 AAAATCGTATAAAATCTCGATTTTTTTTTTTTTTTTTTTTTTTTTTCTCATATTCATATGAAACC 1561  
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 Qy 1562 AGAACATCTGTACTACAACTGTTTAAAGAGGAACTATGTTCTATGAATTA 1621  
 Db 1810 AGAACATCTGTACTACAACTGTTTAAAGAGGAACTATGTTCTATGAATTA 1869  
 Qy 1622 ACTTGTGCTGCTGATAGGACAGACTGGATTTTCAATTTCTTATTAATTTCTGCC 1681  
 Db 1870 ACTTGTGCTGCTGATAGGACAGACTGGATTTTCAATTTCTTATTAATTTCTGCC 1929  
 Qy 1882 ATTTAGAGAGAGAACTACATTTCTATGTTTGAAGAGATTAACCTGAAAGAGAGTGG 1741

Db 1930 ATTTAGAGAGAGAACTACATTTCAATGTTTGAAGAGATTAACCTGAAAGAGAGTGG 1989  
 Qy 1742 CTTTATCTTCACTTTATCGATTAAGTCACTTTATTTGTTTCATTTGTTGATATTTATAT 1801  
 Db 1990 CTTTATCTTCACTTTATCGATTAAGTCACTTTATTTGTTTCATTTGTTGATATTTATAT 2049  
 Qy 1802 CTCTCTTTGACATTAACCTGTTGCTTTTCTAACTTGTGTTAAATATATCTATTTTACC 1861  
 Db 2050 CTCTCTTTGACATTAACCTGTTGCTTTTCTAACTTGTGTTAAATATATCTATTTTACC 2109  
 Qy 1862 AAAGGTATTTAATATTTCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGTAAAT 1921  
 Db 2110 AAAGGTATTTAATATTTCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGTAAAT 2169  
 Qy 1922 TTTTCTAAACAACTTATAGCCAGAGGACAAAGATGATTAATAAATATTTGTTGCC 1981  
 Db 2170 TTTTCTAAACAACTTATAGCCAGAGGACAAAGATGATTAATAAATATTTGTTGCC 2226  
 Qy 1982 CTGGACAAAATAACATGATATNTCCATCCCGAATGCTGCTAGAGTTGGATTAACCTGCA 2041  
 Db 2227 TCTGACAAAATAACATGATATTT-CATTCCTGATGCTGCTAGAGTTAGATTT-AACTGCA 2284  
 Qy 2042 TTTTAAAAAACCCTGAATTTGGGAAGGAANTTGGTAAGTTGGCCAAAANCTTTTGTGAAA 2101  
 Db 2285 TTTTAAAAAACCCTGAATTT---GGAATAGATTTGGTAAGTT---GCAAAGACTTTTGTGAAA 2338  
 Qy 2102 TAATTA 2108  
 Db 2339 TAATTA 2345

## RESULT 6

AAC78582

ID AAC78582 standard; cdna; 2849 BP.

AC AAC78582;

XX 08-FEB-2001 (first entry)

XX Human PRO200 (UNQ174) nucleotide sequence SEQ ID NO:487.

 XX Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;  
 XX expressed sequence tag; detection; cancer; ss.

XX Homo sapiens.

XX WO200053756-A2.

XX 14-SEP-2000.

XX 18-FEB-2000; 2000WO-US04341.

XX 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

XX 29-MAR-1999; 99US-0126773.

XX 21-APR-1999; 99US-0130232.

XX 28-APR-1999; 99US-0131445.

XX 14-MAY-1999; 99US-0134287.

XX 23-JUN-1999; 99US-0141037.

XX 26-JUL-1999; 99US-0145698.

XX 29-OCT-1999; 99US-0162506.

XX 30-NOV-1999; 99WO-US28313.

XX 02-DEC-1999; 99WO-US28551.

XX 02-DEC-1999; 99WO-US28565.

XX 16-DEC-1999; 99WO-US30095.

XX 30-DEC-1999; 99WO-US31243.

XX 30-DEC-1999; 99WO-US31274.

XX 05-JAN-2000; 2000WO-US00219.

XX 06-JAN-2000; 2000WO-US00277.

XX 06-JAN-2000; 2000WO-US00376.

(GETH ) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI; WPI; 2000-611443/58.

DR P-PSDB; AAB44322.

XX Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -

PS Claim 2; Fig 206; 636pp; English.

XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.

XX Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 93.9%; Score 1979.4; DB 21; Length 2849;  
Best Local Similarity 97.7%; Pred. No. 0;  
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

PI	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB; Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ; Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA; Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI; WPI; 2000-611443/58.	QY	602	CTATAACTGCGCTTTAGTACCTTGGAGACCTTTATTCGATATCTTGAACACGAGAGATGCG	661
PI	Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB; Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ; Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA; Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI; WPI; 2000-611443/58.	DB	850	CTATAACTGCGCTTTAGTACCTTGGAGACCTTTATTCGATATCTTGAACACGAGAGATGCG	909
PI	Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ; Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA; Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI; WPI; 2000-611443/58.	QY	662	AGTTGGACCTTAGAGATCTATATAGCCCAACTTGGCAACTCTTGGCAAGGCTTTGTTT	721
PI	Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA; Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI; WPI; 2000-611443/58.	DB	910	AGTTGGACCTTAGAGATCTATATAGCCCAACTTGGCAACTCTTGGCAAGGCTTTGTTT	969
PI	Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI; WPI; 2000-611443/58.	QY	722	TTGGAGAAATCCAGAGTGGTGAACCTTCTAAACGCTGTGGTGGAACTGTGCTGTCTCTCC	781
DR	P-PSDB; AAB44322.	DB	970	TTGGAGAAATCCAGAGTGGTGAACCTTCTAAACGCTGTGGTGGAACTGTGCTGTCTCTCC	1029
XX	Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -	QY	782	GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGAGAACTAAAGAGAACCGATACCA	841
XX	Claim 2; Fig 206; 636pp; English.	DB	1030	GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGAGAACTAAAGAGAACCGATACCA	1089
XX	AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.	QY	842	TTTTCTGGCCAGGTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	901
CC		DB	1090	TTTTCTGGCCAGGTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1149
CC		QY	902	ACAAATGCAATGAATGTCAATGTCTCCAGCAAAAGTTACTTAAATAATACCAAGAGTCC	961
CC		DB	1150	ACAAATGCAATGAATGTCAATGTCTCCAGCAAAAGTTACTTAAATAATACCAAGAGTCC	1209
CC		QY	962	TTCAAGTTGAGACCAAGACCGGTGTCCAGGGAATGCAAAATCACTCACCCAGCTGGCCC	1021
CC		DB	1210	TTCAAGTTGAGACCAAGACCGGTGTCCAGGGAATGCAAAATCACTCACCCAGCTGGCCC	1269
CC		QY	1022	TGAGACCAATGAGAGTGTGACTGTGTGTGAGAGGAGGACACAGAGGATGACCGCATC	1081
CC		DB	1270	TGAGACCAATGAGAGTGTGACTGTGTGTGAGAGGAGGACACAGAGGATGACCGCATC	1329
CC		QY	1082	ACCACACAGAGCTCTTCCACAGAGCTGTCCAGTGTGAGTGGCTGATTTATTTAGAGAACT	1141
CC		DB	1330	ACCACACAGAGCTCTTCCACAGAGCTGTCCAGTGTGAGTGGCTGATTTATTTAGAGAACT	1389
CC		QY	1142	ATGCGTTATCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1201
CC		DB	1390	ATGCGTTATCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1449
CC		QY	1202	TTACAGTGTATCTGAAAGAGGAGACATCAACAGAAATAGAGTTGTGCAACAGCTCTT	1261
CC		DB	1450	TTACAGTGTATCTGAAAGAGGAGACATCAACAGAAATAGAGTTGTGCAACAGCTCTT	1509
CC		QY	1262	TTGAGAGGAGGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGGAAAGAAATTTAAATG	1321
CC		DB	1510	TTGAGAGGAGGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGGAAAGAAATTTAAATG	1569
CC		QY	1322	TTGTATTAATAGATCACCAGCTAGTTTCAGAGTTTACCATGTACCTATTCCTAGCTGG	1381
CC		DB	1570	TTGTATTAATAGATCACCAGCTAGTTTCAGAGTTTACCATGTACCTATTCCTAGCTGG	1629
CC		QY	1382	GTTCTGTATTTTCAGTCTTTCGATAGCGCTTAGGGTAAATGTCTAGTACAGGAAAAAATCTG	1441
CC		DB	1630	GTTCTGTATTTTCAGTCTTTCGATAGCGCTTAGGGTAAATGTCTAGTACAGGAAAAAATCTG	1689
CC		QY	1442	TGCAAGTGTAGACCTGTATTCGCTTGTCTTAACTCTAAAGCTCCATGTCTGGGCT	1501
CC		DB	1690	TGCAAGTGTAGACCTGTATTCGCTTGTCTTAACTCTAAAGCTCCATGTCTGGGCT	1749
CC		QY	1502	AAAACTGTATAAATCTGGATTTTCTGCTCATATTTCTCATATTTGTAATGTAAC	1561
CC		DB	1750	AAAACTGTATAAATCTGGATTTTCTGCTCATATTTCTCATATTTGTAATGTAAC	1809
CC		QY	1562	AGAACATTTCTATGTACTACAAACCTGGTTTAAAAAGGAACTATGTCTATGTAATTA	1621
CC		DB	1810	AGAACATTTCTATGTACTACAAACCTGGTTTAAAAAGGAACTATGTCTATGTAATTA	1869
CC		QY	1622	ACTGTGTCTCTGTATGAGACAGACTGGATTTTCTATTTCTTATTAATGTAATGTA	1681
CC		DB	1870	ACTGTGTCTCTGTATGAGACAGACTGGATTTTCTATTTCTTATTAATGTAATGTA	1929
CC		QY	1682	ATTTAGAGAGAGAGAACTACATTTCTGTTGGAGAGATAAACCTGAAAGAGAGTGG	1741

QY 2 CCCGCGGTGAGTGAAGCTCTACCCCGAGTCAGCAAAATGAGCTCTTCGGGCTTCTCTGG 61

DB 250 CCCGCGGTGAGTGAAGCTCTACCCCGAGTCAGCAAAATGAGCTCTTCGGGCTTCTCTGG 309

QY 62 TGACATCTGCCCTGGCCGCGCAGAGACGAGGAGCTCAGCGGGAATCAACCTGAGTAGTA 121

DB 310 TGACATCTGCCCTGGCCGCGCAGAGACGAGGAGCTCAGCGGGAATCAACCTGAGTAGTA 369

QY 122 AATTCAGTCTTCCAGCAACGAGGACAGACGAGGAGTACAGATCCCTCAGCATGAGAGAA 181

DB 370 AATTCAGTCTTCCAGCAACGAGGACAGACGAGGAGTACAGATCCCTCAGCATGAGAGAA 429

QY 182 TTATTACTGTGTCTACTAATGGAAGTATTCACGCCCAAGGTTTCTCATACTTATCCAA 241

DB 430 TTATTACTGTGTCTACTAATGGAAGTATTCACGCCCAAGGTTTCTCATACTTATCCAA 489

QY 242 GAATACCGTCTTGTATGGAGTATGATGAGTATGAGGAAATGATGATGATGATGATGATGAT 301

DB 490 GAATACCGTCTTGTATGGAGTATGATGAGTATGAGGAAATGATGATGATGATGATGATGAT 549

QY 302 CGTTTGATGAAGATTTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 361

DB 550 CGTTTGATGAAGATTTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 609

QY 362 TAGAAGTTGAGAACCCAGTATGAACTATATAGGCGCTGTGTGTTCTGGTACTG 421

DB 610 TAGAAGTTGAGAACCCAGTATGAACTATATAGGCGCTGTGTGTTCTGGTACTG 669

QY 422 TACAGGAGAAACAGATTTCTAAAGGAAATCAAAATAGGATTAAGATTTGTATCTGATCAAT 481

DB 670 TACAGGAGAAACAGATTTCTAAAGGAAATCAAAATAGGATTAAGATTTGTATCTGATCAAT 729

QY 482 ATTTTCTTCTGAAACAGGTTTCTGATCCACTACAAATTTGTCATGTCACAAATTCACAG 541

DB 730 ATTTTCTTCTGAAACAGGTTTCTGATCCACTACAAATTTGTCATGTCACAAATTCACAG 789

QY 542 AAGCTGTGAGTCTTCAAGTGTACCCCTTCCAGCTTTTCCAGCTGCTGCTTAATG 601

DB 790 AAGCTGTGAGTCTTCAAGTGTACCCCTTCCAGCTTTTCCAGCTGCTGCTTAATG 849

Db 1930 ATTAGAAGAGAACTACATTCATGGTTGGAAGAGATAACCTGAAAGAGAGTG 1989  
 QY 1742 CCTATCTTCACATTTATCGATAGTCAGTTATTTGTTTCATTTGTCATATTTATAT 1801  
 Db 1990 CCTATCTTCACATTTATCGATAGTCAGTTATTTGTTTCATTTGTCATATTTAT 2049  
 QY 1802 CTCCTTTTGACATTAACATGTTGGCTTTCTTAATCTGTTAAATATATCTATTTTACC 1861  
 Db 2050 CTCCTTTTGACATTAACATGTTGGCTTTCTTAATCTGTTAAATATATCTATTTTACC 2109  
 QY 1862 AAGAGTATTTAAATATCTTTTATGACAACTTAGATCAACTATTTTATAGCTTGTAAAT 1921  
 Db 2110 AAGAGTATTTAAATATCTTTTATGACAACTTAGATCAACTATTTTATAGCTTGTAAAT 2169  
 QY 1922 TTTTCTAAACAAATTTGTTATAGCCGAGAGAAACAAAGATGATATAAAATATTTGTCG 1981  
 Db 2170 TTTTCTAAACAAATTTGTTATAGCCGAGAGAAACAAAGATG---ATATAAATATTTGTCG 2226  
 QY 1982 CTGACAAAATACATGTAATNTCCATCCCGAATGGTCTAGAGTTGGATTAAACCTGCA 2041  
 Db 2227 TCTGACAAAATACATGTAATNT---CATCTCGTATGGTCTAGAGTTAGATT---AATCTGCA 2284  
 QY 2042 TTTTAAACAACTGCAATTTGGGAANGGAANTGTTAAGTTGGCCAAANCTTTTTCGAAA 2101  
 Db 2285 TTTTAAACAACTGCAATTT---GGAATAGATTGGTAAAGTT---GCAAAAGACTTTTTCGAAA 2338  
 QY 2102 TAATTTA 2108  
 Db 2339 TAATTTA 2345

## RESULT 7

AAA88515

ID AAA88515 standard; cDNA; 2849 BP.

AC AAA88515;

XX 22-JAN-2001 (first entry)

XX Human PRO200 (VEGF-E) cDNA clone DNA29101-1272.

XX PRO200; vascular epithelial growth factor E; VEGF-E; human;  
 KW ocular disease; retinopathy; maculopathy; therapy;  
 KW retinitis pigmentosa; macular degeneration; retinal detachment;  
 KW retinal tear; macular hole; myopia; traumatic choriorretinopathy;  
 KW acute retinal necrosis syndrome; contusion; edema;  
 KW retinal vision occlusion; vascular disease; retinal vasculitis;  
 KW thrombocytopenic purpura; uveitis; retinal occlusion; ss.

XX Homo sapiens.

OS Key Location/Qualifiers  
 FH 285..1322  
 CD /\*tag= a  
 FT sig\_peptide 285..326  
 FT /\*tag= b  
 FT mat\_peptide 327..1319  
 FT /\*tag= c

XX WO200053760-A2.

XX 14-SEP-2000.

XX 10-MAR-2000; 2000WO-US06319.

XX 12-MAR-1999; 99US-0123957.

XX (GETH ) GENENTECH INC.

XX Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ, Kabakoff RC;  
 PI Klein RD, Kijavini IJ, Kuo SS, La Fleur M, Wood WI;

XX

DR WPI: 2000-587437/55.  
 DR P-PSDB; AAB19578.

XX Novel PRO polypeptides useful for preventing or rescuing retinal cells  
 PT from injury caused by ocular diseases such as retinitis pigmentosa,  
 PT retinopathy, retinal degenerative diseases, degenerative myopia,  
 PT uveitis -

XX Example 8; Fig 1; 140pp; English.

CC The present sequence is that of cDNA clone DNA29101-1272 or UNQ174  
 CC (ATCC 209653) isolated from a human glioma cell line G61 cDNA  
 CC library using probes (see AAA88523-26) based on an expressed sequence  
 CC tag (see AAA88522) identified on the basis of homology to vascular  
 CC endothelial growth factor (VEGF). The clone contains a single open  
 CC reading frame encoding a 345-amino acid protein (see AAB19578)  
 CC designated PRO200 or VEGF-E. The isolated cDNA can be used in the  
 CC recombinant production of PRO200 (VEGF-E). The invention relates  
 CC to the use of PRO polypeptides, including PRO200, to delay, prevent  
 CC or rescue retinal cells such as retinal neurons selected from  
 CC photoreceptors, retinal ganglion cells, displaced retinal ganglion  
 CC cells, amacrine cells, displaced amacrine cells, horizontal and  
 CC bipolar neurons, and supportive cells (including Mueller cells and  
 CC pigment epithelial cells) from injury and degradation. The retinal  
 CC cells are preferably photoreceptors and photoreceptor cell injury or  
 CC death is caused by retinal injury, light or environmental trauma or  
 CC by an ocular disease selected from retinitis pigmentosa, macular  
 CC degeneration, including age-related, retinal detachment, retinal  
 CC tears, retinopathy, retinal degenerative diseases, macular holes,  
 CC degenerative myopia, acute retinal necrosis syndrome, traumatic  
 CC chorioretinopathies or contusion such as Purtscher's retinopathy,  
 CC edema, ischemic conditions such as central or branch retinal vision  
 CC occlusion, collagen vascular diseases, thrombocytopenic purpura,  
 CC uveitis, retinal vasculitis and occlusion associated with Eales  
 CC disease and systemic lupus erythematosus (claimed).

XX Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 93.9%; Score 1979.4; DB 21; Length 2849;  
 Best Local Similarity 97.7%; Pred. No. 0;

Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCCGCCGTGAGTGAGCTCTCACCCAGTCAGCAAAATGAGCTCTTCGGGCTTCTCTGG 61  
 Db 250 CCCGCCGTGAGTGAGCTCTCACCCAGTCAGCAAAATGAGCTCTTCGGGCTTCTCTGG 309  
 QY 62 TGACATCTGCCCTGCGCCGACGAGACGAGGAGCTCAGCGGAATCCCACTGAGTAGTA 121  
 Db 310 TGACATCTGCCCTGCGCCGACGAGACGAGGAGCTCAGCGGAATCCCACTGAGTAGTA 369  
 QY 122 AATTCAGTTTCCAGCAACAGGAACAGAACGAGTCAAGATCCTCAGCATGAGAGAA 181  
 Db 370 AATTCAGTTTCCAGCAACAGGAACAGAACGAGTCAAGATCCTCAGCATGAGAGAA 429  
 QY 182 TTATTACTGTGCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATATCTATCCAA 241  
 Db 430 TTATTACTGTGCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATATCTATCCAA 489  
 QY 242 GAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATCAACTTA 301  
 Db 490 GAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATCAACTTA 549  
 QY 302 CGTTTGATGAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 361  
 Db 550 CGTTTGATGAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 609  
 QY 362 TAGAAGTTGAGGAACCCAGTATGAACTATATATTAGGCGCTGGTGTCTTCTGCTACTG 421  
 Db 610 TAGAAGTTGAGGAACCCAGTATGAACTATATATTAGGCGCTGGTGTCTTCTGCTACTG 669  
 QY 422 TACCAGGAAAACAGATTTTCTAAAGGAAATCAAATTTAGGATAGATTTTGTATCTGATGAAT 481  
 Db 670 TACCAGGAAAACAGATTTTCTAAAGGAAATCAAATTTAGGATAGATTTTGTATCTGATGAAT 729

QY 482 ATTTTCCTTCTGACACAGGGTTCTGCATCCATCAACATTTGTCATGCCACAATTCACAG 541  
 Db |||||  
 QY 730 ATTTTCCTTCTGACACAGGGTTCTGCATCCATCAACATTTGTCATGCCACAATTCACAG 789  
 Db |||||  
 QY 542 AAGCTGTGAGTCTTCAAGTGTCTACCCCTTCACCTTGCCTTGCCTTGAATATG 601  
 Db |||||  
 QY 790 AAGCTGTGAGTCTTCAAGTGTCTACCCCTTCACCTTGCCTTGAATATG 849  
 Db |||||  
 QY 602 CTATTAACCTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACACAGAGATGGC 661  
 Db |||||  
 QY 850 CTATTAACCTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACACAGAGATGGC 909  
 Db |||||  
 QY 662 AGTTGGACCTTAGAAGATCTATATAGGCCAATCTTGGGCACTTCTTGGCAAGCTTTTGT 721  
 Db |||||  
 QY 910 AGTTGGACCTTAGAAGATCTATATAGGCCAATCTTGGGCACTTCTTGGCAAGCTTTTGT 969  
 Db |||||  
 QY 722 TTGGAAGAAATCCAGAGTGTGATCTGAACCTTCTTAAAGAGAGGTAAAGATTATACA 781  
 Db |||||  
 QY 970 TTGGAAGAAATCCAGAGTGTGATCTGAACCTTCTTAAAGAGAGGTAAAGATTATACA 1029  
 Db |||||  
 QY 782 GTCGACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTTAAAGAGAACCGATACCA 841  
 Db |||||  
 QY 1030 GTCGACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTTAAAGAGAACCGATACCA 1089  
 Db |||||  
 QY 842 TTTTCTGGCCAGGTTGTCTCCGTGTAAACGCTGTGTGGGAATCTGTGCTGTCTCTCC 901  
 Db |||||  
 QY 1090 TTTTCTGGCCAGGTTGTCTCCGTGTAAACGCTGTGTGGGAATCTGTGCTGTCTCTCC 1149  
 Db |||||  
 QY 902 ACAATTGCAATGAATGTCAATGTCTCCAGCAAGAAAGTTACTTAAATAATACCAAGAGTCC 961  
 Db |||||  
 QY 1150 ACAATTGCAATGAATGTCAATGTCTCCAGCAAGAAAGTTACTTAAATAATACCAAGAGTCC 1209  
 Db |||||  
 QY 962 TTCAGTTGAGACCAAGACCGTGTCCAGGGATGTCACAAATCACTCACCGAGTGGCCC 1021  
 Db |||||  
 QY 1210 TTCAGTTGAGACCAAGACCGTGTCCAGGGATGTCACAAATCACTCACCGAGTGGCCC 1269  
 Db |||||  
 QY 1022 TGGAGCACCATAGGAGTGTCACTGTGTGTGACAGGGGAGCACAGGAGGATAGCCGCATC 1081  
 Db |||||  
 QY 1270 TGGAGCACCATAGGAGTGTCACTGTGTGTGACAGGGGAGCACAGGAGGATAGCCGCATC 1329  
 Db |||||  
 QY 1082 ACCACACGACCTTCCGACAGCTGTGCAGTGCAGTGGCTGATCTTATAGAACGT 1141  
 Db |||||  
 QY 1330 ACCACACGACCTTCCGACAGCTGTGCAGTGCAGTGGCTGATCTTATAGAACGT 1389  
 Db |||||  
 QY 1142 ATGGTTATCTCCATCTTAATCTCAGTGTGTTCCTTCAAGGACCTTTCATCTTCAGGAT 1201  
 Db |||||  
 QY 1390 ATGGTTATCTCCATCTTAATCTCAGTGTGTTCCTTCAAGGACCTTTCATCTTCAGGAT 1449  
 Db |||||  
 QY 1202 TTACAGTGCATCTGAAGAGGAGACATCAACAGAAATAGGAGTTGTGCAACAGCTCTT 1261  
 Db |||||  
 QY 1450 TTACAGTGCATCTGAAGAGGAGACATCAACAGAAATAGGAGTTGTGCAACAGCTCTT 1509  
 Db |||||  
 QY 1262 TTGAGAGGAGGCTTAAAGACAGGAGAAAGGCTCTCAATCGTGGAAAGAAATTAATG 1321  
 Db |||||  
 QY 1510 TTGAGAGGAGGCTTAAAGACAGGAGAAAGGCTCTCAATCGTGGAAAGAAATTAATG 1569  
 Db |||||  
 QY 1322 TTGATTAATAATAGATCACCACTAGTTTCAGAGTTACATGATGATTCATCTAGCTGG 1381  
 Db |||||  
 QY 1570 TTGATTAATAATAGATCACCACTAGTTTCAGAGTTACATGATGATTCATCTAGCTGG 1629  
 Db |||||  
 QY 1382 GTTCTGTATTTTCAGTCTCTTTCGATACGCTTGTAGGTAATGTCAGTACAGGAAATAAATG 1441  
 Db |||||  
 QY 1630 GTTCTGTATTTTCAGTCTCTTTCGATACGCTTGTAGGTAATGTCAGTACAGGAAATAAATG 1689  
 Db |||||  
 QY 1442 TGAAGTGAAGACCTGATTCGCTTGTCTTAACTTAAAGCTCCATGTCCTGGCCCT 1501  
 Db |||||  
 QY 1690 TGAAGTGAAGACCTGATTCGCTTGTCTTAACTTAAAGCTCCATGTCCTGGCCCT 1749  
 Db |||||  
 QY 1502 AAAATCGTATAAAATCTCGATTTTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTAACC 1561  
 Db |||||  
 QY 1750 AAAATCGTATAAAATCTCGATTTTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTAACC 1809  
 Db |||||

QY 1562 AGAACAATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAATAA 1621  
 Db |||||  
 QY 1810 AGAACAATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAATAA 1869  
 Db |||||  
 QY 1622 ACTTGTGTCRGTCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAATAATTTCTGCC 1681  
 Db |||||  
 QY 1870 ACTTGTGTCRGTCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAATAATTTCTGCC 1929  
 Db |||||  
 QY 1682 ATTTAGAAAGAGAACTACATTCATGTTTGGAGAGATAAACCTGAAAGAGAGATGG 1741  
 Db |||||  
 QY 1930 ATTTAGAAAGAGAACTACATTCATGTTTGGAGAGATAAACCTGAAAGAGAGATGG 1989  
 Db |||||  
 QY 1742 CCTTATCTTCACTTTATCGATAAGTCAAGTTCAGTTTATTTGTTTCAATCTGTACATTTTATATT 1801  
 Db |||||  
 QY 1990 CCTTATCTTCACTTTATCGATAAGTCAAGTTCAGTTTATTTGTTTCAATCTGTACATTTTATATT 2049  
 Db |||||  
 QY 1802 CTCTCTTTTGACATTAATCACTGTTGGCTTTTCTAATCTTGTTPAATAATATATCTATTTTACC 1861  
 Db |||||  
 QY 2050 CTCTCTTTTGACATTAATCACTGTTGGCTTTTCTAATCTTGTTPAATAATATATCTATTTTACC 2109  
 Db |||||  
 QY 1862 AAGGTATTTAATTTCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAAAT 1921  
 Db |||||  
 QY 2110 AAGGTATTTAATTTCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAAAT 2169  
 Db |||||  
 QY 1922 TTTTCTAAACAATTTGTATAGCCAGAGGAACAAAGATGATATAAAATATTTGTTGCC 1981  
 Db |||||  
 QY 2170 TTTTCTAAACAATTTGTATAGCCAGAGGAACAAAGATG--ATATAAATAATTTGTTGCC 2226  
 Db |||||  
 QY 1982 CTGGCAAAATAATACATGATNTCCATCCCGAATGGTCTAGAGTTGGATTAACCTGCA 2041  
 Db |||||  
 QY 2227 TCTGCAAAATAATACATGATNT--CATTCCTGATGGTCTAGAGTTAGAT--AACTGCA 2284  
 Db |||||  
 QY 2042 TTTTAAAAAACCCTGAATTTGGGAAGGAATTTGGTAAGGTTCGCCAACCTTTTGTGAAA 2101  
 Db |||||  
 QY 2285 TTTTAAAAAACCCTGAATTT--GGAATAGAAATTTGTAAGTT--GCAAGACTTTTGTGAAA 2338  
 Db |||||  
 QY 2102 TAATTA 2108  
 Db 2339 TAATTA 2345

## RESULT 8

AAC58579  
 ID AAC58579 standard; cDNA; 2849 BP.

AC AAC58579;  
 DT 29-JAN-2001 (first entry)

DE Human PRO200 protein UNQ174 encoding cDNA SEQ ID NO:1.

Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 dermatological; antiarthritic; antirheumatic; immunosuppressive;  
 haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
 antianaemic; hepatotropic; viricide; antipsoriatic; antiallergic;  
 antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  
 idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 autoimmune thrombocytopenia; immune-mediated renal disease;  
 demyelinating disease; hepatobiliary disease; Whipple's disease;  
 inflammatory bowel disease; gluten-sensitive enteropathy;  
 autoimmune disease; immune-mediated skin disease; allergic disease;  
 immunological disease; transplantation associated disease;  
 graft rejection; graft-versus-host-disease; ss.

Homo sapiens.

WO200053758-A2.

14-SEP-2000.

02-MAR-2000; 2000WO-US05841.

XX PR 08-MAR-1999; 99WO-US05028.  
 PR 10-MAR-1999; 99US-0123618.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 23-MAR-1999; 99US-0125775.  
 PR 12-APR-1999; 99US-0128849.  
 PR 20-APR-1999; 99WO-US08615.  
 PR 28-APR-1999; 99US-0131445.  
 PR 04-MAY-1999; 99US-0132371.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99WO-US04222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30099.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 (GETH) GENENTECH INC.  
 XX PA Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 XX PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 XX PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
 XX DR WPI: 2000-572271/53.  
 XX PS P-PSDB; AAB33414.  
 XX XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX Claim 23; Fig 1; 309pp; English.  
 XX CC The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and

CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;  
 Query Match 93.9%; Score 1979.4; DB 21; Length 2849;  
 Best Local Similarity 97.7%; Pred. No. 0;  
 Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;  
 QY 2 CCGCGCGTGAAGTCTTCAACCCAGTCAGCCAAATAGAGCTCTTGGGCTTCCTCTGG 61  
 DB 250 CCGCGCGTGAAGTCTTCAACCCAGTCAGCCAAATAGAGCTCTTGGGCTTCCTCTGG 309  
 QY 62 TGACATCTGCGCTGGCGCCGAGAGCGAGGAGCTCAGCGGGAATCCACCTGAGTAGTA 121  
 DB 310 TGACATCTGCGCTGGCGCCGAGAGCGAGGAGCTCAGCGGGAATCCACCTGAGTAGTA 369  
 QY 122 AATTCCAGTTTTCCAGCAACAGAGGAGTATGATGAGTATCAAGATCCTCAGCATGAGAGAA 181  
 DB 370 AATTCCAGTTTTCCAGCAACAGAGGAGTATGATGAGTATCAAGATCCTCAGCATGAGAGAA 429  
 QY 182 TTATTTACTGTCTTACTTAATGAGATTTTCAAGCCCAAGGTTTCTCTACTTATCCAA 241  
 DB 430 TTATTTACTGTCTTACTTAATGAGATTTTCAAGCCCAAGGTTTCTCTACTTATCCAA 489  
 QY 242 GAAATACGGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATGATGATGATCAACTTA 301  
 DB 490 GAAATACGGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATGATGATGATCAACTTA 549  
 QY 302 CGTTTGAATGAAGATTTGGGCTTGAAGCCGAGAGATGACATATGCAAGATGATTTTG 361  
 DB 550 CGTTTGAATGAAGATTTGGGCTTGAAGCCGAGAGATGACATATGCAAGATGATTTTG 609  
 QY 362 TAGAAGTTCAGGAACCCAGTGTGAACTATATAGGGCGCTGGTGTGCTTCTGGTACGTG 421  
 DB 610 TAGAAGTTCAGGAACCCAGTGTGAACTATATAGGGCGCTGGTGTGCTTCTGGTACGTG 669  
 QY 422 TACCAGGAAACAGATTTCTAAGGAAATCAAATTAGGATAAGATTTGATCGATGAAT 481  
 DB 670 TACCAGGAAACAGATTTCTAAGGAAATCAAATTAGGATAAGATTTGATCGATGAAT 729  
 QY 482 ATTTTCTCTGAAACCCAGGGTTCTGCATCCATCAACATTTGTCATGCCACATTCACAG 541  
 DB 730 ATTTTCTCTGAAACCCAGGGTTCTGCATCCATCAACATTTGTCATGCCACATTCACAG 789  
 QY 542 AAGCTGTGAGTCTTCCAGTGTCTACCCCTTTCAGCTTTGCACTTGGACCTGCTTAAATAG 601  
 DB 790 AAGCTGTGAGTCTTCCAGTGTCTACCCCTTTCAGCTTTGCACTTGGACCTGCTTAAATAG 849  
 QY 602 CTATAACTGCTTTAGTACCTTGGAAAGACCTTATTCGATATCTTGAAACGAGAGATGGC 661  
 DB 850 CTATAACTGCTTTAGTACCTTGGAAAGACCTTATTCGATATCTTGAAACGAGAGATGGC 909  
 QY 662 AGTTGGACCTTAGAAGATCTATATAGCCCAACTTGGCACTTCTTGCAAGGCTTTTGT 721  
 DB 910 AGTTGGACCTTAGAAGATCTATATAGCCCAACTTGGCACTTCTTGCAAGGCTTTTGT 969  
 QY 722 TTGGAAGAAATCCAGAGTGGTGGATCTGAACTTCTAAGAGAGGTAAGATTATACA 781  
 DB 970 TTGGAAGAAATCCAGAGTGGTGGATCTGAACTTCTAAGAGAGGTAAGATTATACA 1029  
 QY 782 GCTGCACACTCGTAACCTTCTCAGTGTCCATAGGAGGAACTAAGAGAACCGATACA 841  
 DB 1030 GCTGCACACTCGTAACCTTCTCAGTGTCCATAGGAGGAACTAAGAGAACCGATACA 1089  
 QY 842 TTTTCTGGCCAGGTTGTCTCTCTGGTTAAACGCTGTGGTGGGAACTGTGCTGTCTCTCC 901  
 DB 1090 TTTTCTGGCCAGGTTGTCTCTCTGGTTAAACGCTGTGGTGGGAACTGTGCTGTCTCTCC 1149  
 QY 902 ACAATTGCAATGAATGCTCAATGTGTCCCAAGCAAGATTTACTAAAAATACCAAGAGGTC 961  
 DB 1150 ACAATTGCAATGAATGCTCAATGTGTCCCAAGCAAGATTTACTAAAAATACCAAGAGGTC 1209



QY 962 TTCAGTTGACCAAGACCGGTGTGTCAGGGATTGCACAAATCACTCACGAGCTGGCCC 1021  
DB 1210 TTCAGTTGACCAAGACCGGTGTGTCAGGGATTGCACAAATCACTCACGAGCTGGCCC 1269  
QY 1022 TGGAGCACCATGAGGAGTGTGATGTGTGTGTCAGGGAGCAACAGGAGATACCCGATC 1081  
DB 1270 TGGAGCACCATGAGGAGTGTGATGTGTGTGTCAGGGAGCAACAGGAGATACCCGATC 1329  
QY 1082 ACCACAGAGAGCTCTTCCACAGAGCTGTGTCAGTGCAGTGCATCTATTATAGAACGT 1141  
DB 1330 ACCACAGAGAGCTCTTCCACAGAGCTGTGTCAGTGCAGTGCATCTATTATAGAACGT 1389  
QY 1142 ATCGGTATCTCCATCCTTAATCTCAGTGTGTTGCTTCAAGGACCTTTCATCTTCAGGAT 1201  
DB 1390 ATCGGTATCTCCATCCTTAATCTCAGTGTGTTGCTTCAAGGACCTTTCATCTTCAGGAT 1449  
QY 1202 TTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTAGGAGTGTGCAACAGCTCTT 1261  
DB 1450 TTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTAGGAGTGTGCAACAGCTCTT 1509  
QY 1262 TTTGAGAGGAGGCTTAAAGGACAGGAAAAAGGCTTCAATCGTGGAAAGAAAAATTAAATG 1321  
DB 1510 TTTGAGAGGAGGCTTAAAGGACAGGAAAAAGGCTTCAATCGTGGAAAGAAAAATTAAATG 1569  
QY 1322 TTGTATTAATAGATCAACAGCTAGTTCAGAGTTACCATGTACGTATTCACCTAGCTGG 1381  
DB 1570 TTGTATTAATAGATCAACAGCTAGTTCAGAGTTACCATGTACGTATTCACCTAGCTGG 1629  
QY 1382 GTTCTGTATTTCAAGTCTTTCGATAGCGCTTACGGTAACTGTCAGTACGGAAGAAACCTG 1441  
DB 1630 GTTCTGTATTTCAAGTCTTTCGATAGCGCTTACGGTAACTGTCAGTACGGAAGAAACCTG 1689  
QY 1442 TGAAGTGAAGCCTGATTCCTGCTTGCCTTTAACTCTAAAGCTCCATGCTCTGGGCTT 1501  
DB 1690 TGAAGTGAAGCCTGATTCCTGCTTGCCTTTAACTCTAAAGCTCCATGCTCTGGGCTT 1749  
QY 1502 AAAATCGTAAATCTGAGTATTTTCTGCTTCAATCTTCTTAAATTTCTGCTG 1561  
DB 1750 AAAATCGTAAATCTGAGTATTTTCTGCTTCAATCTTCTTAAATTTCTGCTG 1809  
QY 1562 AGAACATCTATCTACTACAACTGCTTTTAAAGGAACTATGCTGCTATGAATTA 1621  
DB 1810 AGAACATCTATGATCTACAACTGCTTTTAAAGGAACTATGCTGCTATGAATTA 1669  
QY 1622 ACTTGTCTCTGTGATGAGACAGCTGGAATTTTCTATTTCTTAAATTTCTGCTG 1681  
DB 1870 ACTTGTCTCTGTGATGAGACAGCTGGAATTTTCTATTTCTTAAATTTCTGCTG 1929  
QY 1682 ATTTAGAGAGAGAACTACATTCATGCTTTTGAAGAGATAAACCCTGAAAGAGAGTGG 1741  
DB 1930 ATTTAGAGAGAGAACTACATTCATGCTTTTGAAGAGATAAACCCTGAAAGAGAGTGG 1989  
QY 1742 CCTTATCTTTCACCTTATCGATAAGTCAAGTATTTGTTTCAATGCTGACATTTTATATT 1801  
DB 1990 CCTTATCTTTCACCTTATCGATAAGTCAAGTATTTGTTTCAATGCTGACATTTTATATT 2049  
QY 1802 CTCCTTTTGACATTAATACCTGTTGGCTTTTCTAATCTTGTAAATATATCTATTTTACC 1861  
DB 2050 CTCCTTTTGACATTAATACCTGTTGGCTTTTCTAATCTTGTAAATATATCTATTTTACC 2109  
QY 1862 AAGGTATTTTAAATCTTTTATGACACTTATGATCACTATTTTATGCTGTTGTAAT 1921  
DB 2110 AAGGTATTTTAAATCTTTTATGACACTTATGATCACTATTTTATGCTGTTGTAAT 2169  
QY 1922 TTTTCTAAAACAAATTTGTTATAGCCAGAGAAACAAAGATGATGATATAAATATTTGTC 1981  
DB 2170 TTTTCTAAAACAAATTTGTTATAGCCAGAGAAACAAAGATG--ATATAAATATTTGTC 2226  
QY 1982 CTGCAAAAATACATGATNTCCATCCCGAATGCTGCTAGAGTTGGATTAACCTGCA 2041  
DB 2227 TCTGCAAAAATACATGATNTT--CAATCTCGTATGCTGCTAGAGTTAGATT--AATCTGCA 2284  
QY 2042 TTTTAAAACCTGAATTCGGAAGGAANTTGTAGGTTGGCAANCTTTTGA 2101

DB 2285 TTTTAAAAAAGTGAATTT--GGAATAGAATTTGTAAGTT--GCAAAAGACTTTTGA 2338  
QY 2102 TAATTAA 2108  
DB 2339 TAATTAA 2345  
RESULT 9  
AAA77621  
ID AAA77621 standard; cDNA; 2849 BP.  
XX  
AC AAA77621;  
XX  
DT 07-NOV-2000 (first entry)  
XX  
DE Human PRO713 cDNA sequence SEQ ID NO:136.  
XX  
KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
KW cytostatic; gene therapy; vaccine; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200032221-A2.  
XX  
PD 08-JUN-2000.  
XX  
PF 30-NOV-1999; 99WO-US28313.  
XX  
PR 01-DEC-1998; 98WO-US25108.  
PR 16-DEC-1998; 98US-0112850.  
PR 12-JAN-1999; 99US-0115554.  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 28-APR-1999; 99US-0131445.  
PR 14-MAY-1999; 99WO-US12252.  
PR 02-JUN-1999; 99US-0141037.  
PR 23-JUN-1999; 99US-0144758.  
PR 20-JUL-1999; 99US-0145698.  
PR 26-JUL-1999; 99WO-US20111.  
PR 01-SEP-1999; 99WO-US20594.  
PR 08-SEP-1999; 99WO-US20944.  
PR 13-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-OCT-1999; 99US-0162506.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;  
PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;  
PI Matanabe CK, Williams PM, Wood WI;  
XX  
DR WPI; 2000-412154/35.  
DR P-PSDB; AAB24412.  
XX  
PT Nucleic acids encoding PRO polypeptides useful for preventing,  
PT diagnosing and treating atherosclerosis, endothelial or  
PT angiogenic disorders in mammals -  
XX  
PS Claim 61; Fig 49; 315pp; English.  
XX  
CC The present invention describes nucleic acids encoding PRO polypeptides  
CC useful for preventing, diagnosing and treating atherosclerosis  
CC cardiovascular, endothelial or angiogenic disorder in mammals by  
CC modulating cell proliferation, angiogenesis and cardiovascularisation,  
CC and for identifying agonists and antagonists of these processes. The  
CC nucleic acids and the proteins they encode may be used in the  
CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate PRO expression such as cardiovascular, endothelial or

CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and  
 CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors  
 CC containing them and the PRO polypeptide may be used to treat disorders  
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and  
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in  
 CC the exemplification of the present invention.

XX SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;  
 Query Match 93.9%; Score 1979.4; DB 21; Length 2849;  
 Best Local Similarity 97.7%; Pred. No. 0;  
 Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;  
 QY 2 CCGCCGTGAGTGGCTCTCACCCAGTCAGCCAAATGAGCCCTTCGCGCTTCCTCGG 61  
 DB 250 CCGCCGTGAGTGGCTCTCACCCAGTCAGCCAAATGAGCCCTTCGCGCTTCCTCGC 309  
 QY 62 TGACATCTGCCCTGGCCGCGCAGAGAGCGGAGTCTCAGCGGAATCCAACTGAGTAGTA 121  
 DB 310 TGACATCTGCCCTGGCCGCGCAGAGACAGGGGACTCAGCGGAATCCAACTGAGTAGTA 369  
 QY 122 AATTCAGTTTCCAGCAACAGGACAGAACCGGTACAGATCCTCAGCATGAGAGAA 181  
 DB 370 AATTCAGTTTCCAGCAACAGGACAGAACCGGTACAGATCCTCAGCATGAGAGAA 429  
 QY 182 TTATTACTGTCTTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTACTTATCCAA 241  
 DB 430 TTATTACTGTCTTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTACTTATCCAA 489  
 QY 242 GAAATACGGTCTGGTATGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAACTTA 301  
 DB 490 GAAATACGGTCTGGTATGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAACTTA 549  
 QY 302 GCTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTG 361  
 DB 550 GCTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTG 609  
 QY 362 TAGAAGTTGAGGAACCCAGTGGTGAATATATATAGGGCGCTGGTGTCTGTTACTG 421  
 DB 610 TAGAAGTTGAGGAACCCAGTGGTGAATATATATAGGGCGCTGGTGTCTGTTACTG 669  
 QY 422 TACCAGGAACACAGATTTCTAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 481  
 DB 670 TACCAGGAACACAGATTTCTAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 729  
 QY 482 ATTTCTCTTGAACCGGGTTTGGATCCATCAACATGTGTCAGCCCAATTCACAG 541  
 DB 730 ATTTCTCTTGAACCGGGTTTGGATCCATCAACATGTGTCAGCCCAATTCACAG 789  
 QY 542 AAGCTGTGAGTCTTCAAGTGTACCCCTTCCAGCTTTGCCACTGGACCTGCTTAATAATG 601  
 DB 790 AAGCTGTGAGTCTTCAAGTGTACCCCTTCCAGCTTTGCCACTGGACCTGCTTAATAATG 849  
 QY 602 CTATACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCCAGAGATGGC 661  
 DB 850 CTATACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCCAGAGATGGC 909  
 QY 662 AGTTGGACTTGAAGATCTATATAGGCAACTTGGCAACTTCTTGGCAAGCTTTTGT 721  
 DB 910 AGTTGGACTTGAAGATCTATATAGGCAACTTGGCAACTTCTTGGCAAGCTTTTGT 969  
 QY 722 TTGGAAGAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGAGGTAAATATACA 781  
 DB 970 TTGGAAGAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGAGGTAAATATACA 1029  
 QY 782 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAGAACTAAAGAGAACCGATACCA 841  
 DB 1030 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAGAACTAAAGAGAACCGATACCA 1089  
 QY 842 TTTTCTGGCCAGGTTGTCTCTCGTTAAACCGCTGTGGTGGAACTGTGCTGTGCTCC 901  
 DB 1090 TTTTCTGGCCAGGTTGTCTCTCGTTAAACCGCTGTGGTGGAACTGTGCTGTGCTCC 1149

QY 902 ACATTTGCAATGATGTCAATGTGTCCAGCAAGAGTTACTAAAAATACACAGAGTCC 961  
 DB 1150 ACATTTGCAATGATGTCAATGTGTCCAGCAAGAGTTACTAAAAATACACAGAGTCC 1209  
 QY 962 TTCAAGTTGAGACCAAGACCGGTGTCTAGGGGATTTGCAAAATCACTCACCGAGTGGCCC 1021  
 DB 1210 TTCAAGTTGAGACCAAGACCGGTGTCTAGGGGATTTGCAAAATCACTCACCGAGTGGCCC 1269  
 QY 1022 TGGAGACCAATGAGGAGTGTGACTGTGTGTCAGAGGGAGCAGAGAGGATACCCGATC 1081  
 DB 1270 TGGAGACCAATGAGGAGTGTGACTGTGTGTCAGAGGGAGCAGAGAGGATACCCGATC 1329  
 QY 1082 ACCACCAAGAGCTCTTCCCCAGAGCTGTGTCAGTGCAGTGGCTGATTTCTATTAGAGAACGT 1141  
 DB 1330 ACCACCAAGAGCTCTTCCCCAGAGCTGTGTCAGTGCAGTGGCTGATTTCTATTAGAGAACGT 1389  
 QY 1142 ATGGTTATCTCATCTTAAATCTCAGTGTGTGTTTCTTCAAGGACCTTCTCATCTCAGGAT 1201  
 DB 1390 ATGGTTATCTCATCTTAAATCTCAGTGTGTGTTTCTTCAAGGACCTTCTCATCTCAGGAT 1449  
 QY 1202 TTACAGTGCATTTCTGAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCTCTT 1261  
 DB 1450 TTACAGTGCATTTCTGAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCTCTT 1509  
 QY 1262 TTGAGAGAGGCCCTAAAGGACAGGAGAAAGGCTCTTCAATCTGCGGAAAGAAATTAATG 1321  
 DB 1510 TTGAGAGAGGCCCTAAAGGACAGGAGAAAGGCTCTTCAATCTGCGGAAAGAAATTAATG 1569  
 QY 1322 TTGTATTAATAGATCACCAGTATGTTTCAAGTGTACATGTACGTATTCACCTAGCTGG 1381  
 DB 1570 TTGTATTAATAGATCACCAGTATGTTTCAAGTGTACATGTACGTATTCACCTAGCTGG 1629  
 QY 1382 GTTCTGATTTTCAAGTCTTTCGATACCGCTTAGGGTAAATGTCTAGTACAGGAAAAAACTG 1441  
 DB 1630 GTTCTGATTTTCAAGTCTTTCGATACCGCTTAGGGTAAATGTCTAGTACAGGAAAAAACTG 1689  
 QY 1442 TGCAAGTGTAGCACCTGATTCGCTTGCCTTAACTCTAAAGCTCCATGTCCTGGGCT 1501  
 DB 1690 TGCAAGTGTAGCACCTGATTCGCTTGCCTTAACTCTAAAGCTCCATGTCCTGGGCT 1749  
 QY 1502 AAAATCGTATAAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTCTCATATTCACATATGAAACC 1561  
 DB 1750 AAAATCGTATAAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTCTCATATTCACATATGAAACC 1809  
 QY 1562 AGACATTTCTATGTACTACAAACCTGTTTAAAGAGGACTATGTCGTATGAATAA 1621  
 DB 1810 AGACATTTCTATGTACTACAAACCTGTTTAAAGAGGACTATGTCGTATGAATAA 1869  
 QY 1622 ACTTGTGTCRTGCTGATAGGACAGACTGGATTTTTTCTCATATTTCTTATTAATAATTTCTGCC 1681  
 DB 1870 ACTTGTGTCRTGCTGATAGGACAGACTGGATTTTTTCTCATATTTCTTATTAATAATTTCTGCC 1929  
 QY 1682 ATTTAGAGAGAGAGACCTACATTCATGTTGGAGAGATAAACCTGAAAGAGAGTGG 1741  
 DB 1930 ATTTAGAGAGAGAGACCTACATTCATGTTGGAGAGATAAACCTGAAAGAGAGTGG 1989  
 QY 1742 CTTATCTTCACTTTATCGATAAGTCAAGTTTAAATTTTCTTCAATGTGTACATTTTATATT 1801  
 DB 1990 CTTATCTTCACTTTATCGATAAGTCAAGTTTAAATTTTCTTCAATGTGTACATTTTATATT 2049  
 QY 1802 CTCCTTTTGACATTAATACTGTTGGCTTTCTAATCTTGTAAATATATATCTATTTTACC 1861  
 DB 2050 CTCCTTTTGACATTAATACTGTTGGCTTTCTAATCTTGTAAATATATATCTATTTTACC 2109  
 QY 1862 AAAGGTATTTAATTTCTTTTATGACACTTATAGATCAACTTTTCTTTTCTGCTGGTAAAT 1921  
 DB 2110 AAAGGTATTTAATTTCTTTTATGACACTTATAGATCAACTTTTCTTTTCTGCTGGTAAAT 2169  
 QY 1922 TTTTCTAAACCAATTTGTTATAGCCAGAGGAAACAGATGATATAAATAATTTGTTGCC 1981  
 DB 2170 TTTTCTAAACCAATTTGTTATAGCCAGAGGAAACAGATG---ATAAATAATTTGTTGC 2226  
 QY 1982 CTGGACAAAAATACATGTATNTCCATCCGGAATGGTGTAGAGTGGATTAACCTGCA 2041

Db 2227 TCTGACAAAATACATGTAATT-CAATCTCGTATGGTGTAGATTAGATT-AATCTGCA 2284  
 QY 2042 TTTTAAAAAACCCTGAATGGGAANGGAANTGGTAAGTTGGCCAAANCTTTTGTGAAA 2101  
 Db 2285 TTTTAAAAAACCCTGAATGGGAANGGAANTGGTAAGTTGGCCAAANCTTTTGTGAAA 2338  
 QY 2102 TAAATTA 2108  
 Db 2339 TAAATTA 2345

## RESULT 10

AAS21386  
 ID AAS21386 standard; cDNA; 2849 BP.

XX AAS21386;  
 AC AAS21386;

DT 24-OCT-2001 (first entry)

XX Human cDNA sequence encoding for PRO200 polypeptide.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.

XX Homo sapiens.

XX WO2001140466-A2.

XX 07-JUN-2001.

PF 01-DEC-2000; 2000WO-US32678.

PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28634.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 20-DEC-1999; 99WO-US30999.

PR 30-DEC-1999; 99WO-US31243.

PR 06-JAN-2000; 2000WO-US00277.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.

PR 01-MAR-2000; 2000WO-US05601.

PR 20-MAR-2000; 2000WO-US07377.

PR 21-MAR-2000; 2000WO-US07532.

PR 20-MAR-2000; 2000WO-US08439.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 10-NOV-2000; 2000WO-US30873.

XX (GETH ) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-408281/43.

DR P-PSDB; AAU12314.

XX Isolated, secretory and transmembrane PRO polypeptide used to detect

PT other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical  
 XX Claim 3; Fig 285; 813pp; English.  
 XX AAS21244-AAS21518 encode for novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, the release of a cytokine from peripheral blood  
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.  
 XX Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;  
 SQ

Query Match 93.9%; Score 1979.4; DB 22; Length 2849;  
 Best Local Similarity 97.7%; Pred. No. 0;  
 Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCGCGCGTGGAGTCTCTCACCCAGTCAGCAAAATGAGCTCTTCGGGCTTCCTGG 61  
 Db 250 CCGCGCGTGGAGTCTCTCACCCAGTCAGCAAAATGAGCTCTTCGGGCTTCCTGG 309  
 QY 62 TGACATCTGCTCCCTGGCCGAGAGCGAGGACTCAGCGGAAATCCAACTGAGTAGTA 121  
 Db 310 TGACATCTGCTCCCTGGCCGAGAGCGAGGACTCAGCGGAAATCCAACTGAGTAGTA 369  
 QY 122 AATTCAGTTTCCAGCAACAGGACAGAGCGAGTACAGATCCTCAGCATGAGAGAA 181  
 Db 370 AATTCAGTTTCCAGCAACAGGACAGAGCGAGTACAGATCCTCAGCATGAGAGAA 429  
 QY 182 TTATTACTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCATCTATCCAA 241  
 Db 430 TTATTACTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCATCTATCCAA 489  
 QY 242 GAAATACGCTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATCAACTTA 301  
 Db 490 GAAATACGCTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATCAACTTA 549  
 QY 302 CGTTTGAATGAAGATTGGGCTTGAAGACCCAGAGAGATGACATATGCAAGTATGATTTTG 361  
 Db 550 CGTTTGAATGAAGATTGGGCTTGAAGACCCAGAGAGATGACATATGCAAGTATGATTTTG 609  
 QY 362 TAGAGTTGAGGAAACCCAGTATGGAACATATATTAGGCGCTGGTGTGTTCTGTTACTG 421  
 Db 610 TAGAGTTGAGGAAACCCAGTATGGAACATATATTAGGCGCTGGTGTGTTCTGTTACTG 669  
 QY 422 TACCAGGAAACAGATTTCTTAAGGAAATCAAAATAGGATAGATTTGTATCTGATGAAT 481  
 Db 670 TACCAGGAAACAGATTTCTTAAGGAAATCAAAATAGGATAGATTTGTATCTGATGAAT 729  
 QY 482 ATTTCTCTTCTGAACCCAGGGTTCTGTCATCCACTACAAATTTCTATGCCACAATTCACAG 541  
 Db 730 ATTTCTCTTCTGAACCCAGGGTTCTGTCATCCACTACAAATTTCTATGCCACAATTCACAG 789  
 QY 542 AAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCCACTGACCTGCTTAATATG 601  
 Db 790 AAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCCACTGACCTGCTTAATATG 849

QY 602 CTATACTGCTTTAGTACCTTGAAGACCTTATTGATATCTGTGAACGAGAGATGCG 661  
Db 850 CTATAA CTGCTTTAGTACCTTGAAGACCTTATTGATATCTGTGAACGAGAGATGCG 909  
QY 662 AGTTGGACTTAGAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGT 721  
Db 910 AGTTGGACTTAGAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTGT 969  
QY 722 TTGAAGAAATCCAGAGTGTGATCTGAACCTTCTAAAGAGAGAGTAAAGATTATACA 781  
Db 970 TTGAAGAAATCCAGAGTGTGATCTGAACCTTCTAAAGAGAGAGTAAAGATTATACA 1029  
QY 782 GCTGCACACTCGTAACTTCTCAGTGTCCATAAGGGAGAACTAAAGAGAACCGATACCA 841  
Db 1030 GCTGCACACTCGTAACTTCTCAGTGTCCATAAGGGAGAACTAAAGAGAACCGATACCA 1089  
QY 842 TTTTCTGGCCAGGTGTCTCTGTTTAAACGCTGTGTGGGAACTGTGCTGTGTCTCC 901  
Db 1090 TTTTCTGGCCAGGTGTCTCTGTTTAAACGCTGTGTGGGAACTGTGCTGTGTCTCC 1149  
QY 902 ACAATTGCAATGAATGTCAATGTCTCCCAAGCAAGTACTTAAATAATACCAAGGTCC 961  
Db 1150 ACAATTGCAATGAATGTCTCCCAAGCAAGTACTTAAATAATACCAAGGTCC 1209  
QY 962 TTCAAGTTGAGACCAAGACCGGTGTGAGGGGATTCACAAATCACTCACCGACGTGGCCC 1021  
Db 1210 TTCAAGTTGAGACCAAGACCGGTGTGAGGGGATTCACAAATCACTCACCGACGTGGCCC 1269  
QY 1022 TGGAGCACCATGAGAGTGTCACTGTGTGTCAGAGGAGACACAGGAGGATCCGCGATC 1081  
Db 1270 TGGAGCACCATGAGAGTGTCACTGTGTGTCAGAGGAGACACAGGAGGATCCGCGATC 1329  
QY 1082 ACCACAGCAGCTCTTGGCCAGAGCTGTGSCAGTGCAGTGGCTGATTCTATTAGAACGCT 1141  
Db 1330 ACCACAGCAGCTCTTGGCCAGAGCTGTGSCAGTGCAGTGGCTGATTCTATTAGAACGCT 1389  
QY 1142 ATGCTTATCTCATCTTAACTCACTGTTTTCCTTCAAGGACCTTTCATCTTCAGGAT 1201  
Db 1390 ATGCTTATCTCATCTTAACTCACTGTTTTCCTTCAAGGACCTTTCATCTTCAGGAT 1449  
QY 1202 TTACAGTGCATTCTGAAAGAGAGACATCAACAGAAATTAGAGTGTGCAACAGCTCTT 1261  
Db 1450 TTACAGTGCATTCTGAAAGAGAGACATCAACAGAAATTAGAGTGTGCAACAGCTCTT 1509  
QY 1262 TTGAGAGAGGCTTAAAGGACAGAGAAAGAGTCTTCAATCGTGGAAAGAAATTAATG 1321  
Db 1510 TTGAGAGAGGCTTAAAGGACAGAGAAAGAGTCTTCAATCGTGGAAAGAAATTAATG 1569  
QY 1322 TTGATTAATAATAGATCACCAGCTAGTGTTCAGAGTTTACCATGTAGCTATTCCACTAGCTGG 1381  
Db 1570 TTGATTAATAATAGATCACCAGCTAGTGTTCAGAGTTTACCATGTAGCTATTCCACTAGCTGG 1629  
QY 1382 GTTCTGTATTTCACTTTCTTTCGATCGGCTTAGGGTAAATGTCAGTACAGGAAATAAATG 1441  
Db 1630 GTTCTGTATTTCACTTTCTTTCGATCGGCTTAGGGTAAATGTCAGTACAGGAAATAAATG 1689  
QY 1442 TCGAGTGCAGACCTGATTTCGTTGCTTCTTAACTTAAAGCTTCAAGTTCCTGCGGCT 1501  
Db 1690 TCGAGTGCAGACCTGATTTCGTTGCTTCTTAACTTAAAGCTTCAAGTTCCTGCGGCT 1749  
QY 1502 AAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTA 1561  
Db 1750 AAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTA 1809  
QY 1562 AGACATCTTATGTACTCAACCTGTTTTTAAAGGAACTATGTTCTATCAATTA 1621  
Db 1810 AGACATCTTATGTACTCAACCTGTTTTTAAAGGAACTATGTTCTATCAATTA 1869  
QY 1622 ACTGTGTCCTGATAGGACAGACTGATTTTTCATATTTCTTATTAATAATTTCTGCC 1681  
Db 1870 ACTGTGTCCTGATAGGACAGACTGATTTTTCATATTTCTTATTAATAATTTCTGCC 1929  
QY 1682 ATTTAGAGAGAGAACTACATTCACTGTGTTTGAAGAGATTAACCTGAAAGAGAGTGG 1741

Db 1930 ATTTAGAGAGAGAACTACATTCAAGTTTGAAGAGATTAACCTGAAAGAGAGTGG 1989  
QY 1742 CTTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCAATTTGTGTACATTTTATAT 1801  
Db 1990 CTTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCAATTTGTGTACATTTTATAT 2049  
QY 1802 CTCCTTTTGAATTAATTAATCTGCTTTCTTAATCTTGTAAATATATATCTATTTTACC 1861  
Db 2050 CTCCTTTTGAATTAATTAATCTGCTTTCTTAATCTTGTAAATATATATCTATTTTACC 2109  
QY 1862 AAAGGTATTTAATATTTCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGTGTAAT 1921  
Db 2110 AAAGGTATTTAATATTTCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGTGTAAT 2169  
QY 1922 TTTTCTAAACACAAATTTATAGCCAGAGAACAAAGATGATATAAATAATTTGTTGCC 1981  
Db 2170 TTTTCTAAACACAAATTTATAGCCAGAGAACAAAGATG---ATATATAATATTTGTTGCC 2226  
QY 1982 CTGACAAAAATACATGATATNTCCATCCCGAATGCTGTAGAGTTGGATTAAACCTGCA 2041  
Db 2227 TCTGACAAAAATACATGATATTT-CATTCTCGTATGCTGTAGAGTTAGATT-AATCTGCA 2284  
QY 2042 TTTTAAAAAACTGAAATTTGGGAAGGAATTTGTAAGTTGGCCAAACCTTTTGTGAAA 2101  
Db 2285 TTTTAAAAAACTGAAAT---GGAATAGAAATTTGGTAAGTT---GCAAGAGACTTTTGTGAAA 2338  
QY 2102 TAATTA 2108  
Db 2339 TAATTA 2345

RESULT 11  
AAC90564  
ID AAC90564 standard; cDNA; 2849 BP.  
XX  
AC AAC90564;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
Human PRO200 cDNA.  
XX  
Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;  
vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
vulnerable; angiogenic; gene therapy; cardiovascular disease;  
endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
wound healing; ss.  
XX  
Homo sapiens.  
XX  
OS  
PN WO200073445-A2.  
XX  
PD 07-DEC-2000.  
XX  
PF 17-MAY-2000; 2000WO-US13705.  
XX  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.





Db 1030 GCTGCACACCTCGTAATCTTCTCAGTGTCCATAAGGAAGAACTAAAGAGAACCGATACCA 1089  
QY 842 TTTTCTGGCAGCTGCTCCCTGTTAAACGCTGTGGTGGAACTGTGCTGTGCTCC 901  
Db 1090 TTTTCTGGCAGCTGCTCCCTGTTAAACGCTGTGGTGGAACTGTGCTGTGCTCC 1149  
QY 902 ACAATTGCAATGAATGTCAATGTGTCCTCAAGCAAAAGTTACTAAAAATACCAAGAGTCC 961  
Db 1150 ACAATTGCAATGAATGTCAATGTGTCCTCAAGCAAAAGTTACTAAAAATACCAAGAGTCC 1209  
QY 962 TTCAGTTGAGACCAAGACCGGTGTGTCAGGGATTGCAAAATCACTCAAGAGTGGCC 1021  
Db 1210 TTCAGTTGAGACCAAGACCGGTGTGTCAGGGATTGCAAAATCACTCAAGAGTGGCC 1269  
QY 1022 TGGAGCACCATGAGAGTGTGACTGTGTGAGAGGAGACAGGAGATAGCCGATC 1081  
Db 1270 TGGAGCACCATGAGAGTGTGACTGTGTGAGAGGAGACAGGAGATAGCCGATC 1329  
QY 1082 ACCACAGAGCTCTTGGCCAGAGCTGTGAGTGCAGTGGCTGATTTATTAGAGAACT 1141  
Db 1330 ACCACAGAGCTCTTGGCCAGAGCTGTGAGTGCAGTGGCTGATTTATTAGAGAACT 1389  
QY 1142 ATGCGTTATCTCCATCTTAATCTCAGTTGTTGCTTCAAGACCTTTTCATCTCAGAT 1201  
Db 1390 ATGCGTTATCTCCATCTTAATCTCAGTTGTTGCTTCAAGACCTTTTCATCTCAGAT 1449  
QY 1202 TTACAGTGCATTCTGAAAGAGAGACATCAAAACAGAAATAGGAGTTGTCAACAGCTCT 1261  
Db 1450 TTACAGTGCATTCTGAAAGAGAGACATCAAAACAGAAATAGGAGTTGTCAACAGCTCT 1509  
QY 1262 TTGAGAGAGGCTTAAAGACAGGAGAAAGTCTTCAATCTGTGGAAGAAATTAATG 1321  
Db 1510 TTGAGAGAGGCTTAAAGACAGGAGAAAGTCTTCAATCTGTGGAAGAAATTAATG 1569  
QY 1322 TTGTTATTAATAGATACACAGCTAGTTTCAGAGTTTACCATGACGTATTCCTAGCTGG 1381  
Db 1570 TTGTTATTAATAGATACACAGCTAGTTTCAGAGTTTACCATGACGTATTCCTAGCTGG 1629  
QY 1382 GTTCTGTATTTTCAGTTCTTTTCGATAGCGCTTAGGGTAAATGTCACTACAGAAAAAATG 1441  
Db 1630 GTTCTGTATTTTCAGTTCTTTTCGATAGCGCTTAGGGTAAATGTCACTACAGAAAAAATG 1689  
QY 1442 TGCAAGTGAACCTGATTCCTGCTGCTTAATCTTAAAGCTCCATGTCTGGGCT 1501  
Db 1690 TGCAAGTGAACCTGATTCCTGCTGCTTAATCTTAAAGCTCCATGTCTGGGCT 1749  
QY 1502 AAAATCGTATAAAATCTGGAATTTTTTTTTTTTGTCTCATATTCATATATGTAAC 1561  
Db 1750 AAAATCGTATAAAATCTGGAATTTTTTTTTTTTGTCTCATATTCATATATGTAAC 1809  
QY 1562 AGAATCTATGTACTACAAACCTGGTTTTTAAAGAACTATGTGCTATGAATTA 1621  
Db 1810 AGAATCTATGTACTACAAACCTGGTTTTTAAAGAACTATGTGCTATGAATTA 1869  
QY 1622 ACTTGTGCTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAATTTCTGCC 1681  
Db 1870 ACTTGTGCTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAATTTCTGCC 1929  
QY 1682 ATTTAGAGAGAGAACTACATTTTCATGTTTGGAAAGAGATAAACCCTGAAAGAGAGTGG 1741  
Db 1930 ATTTAGAGAGAGAACTACATTTTCATGTTTGGAAAGAGATAAACCCTGAAAGAGAGTGG 1989  
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QY 1802 CTCCTTTTGACATTAATGCTGTTGCTTTTCAATCTTGTGTAATATCTATTTTACC 1861  
Db 2050 CTCCTTTTGACATTAATGCTGTTGCTTTTCAATCTTGTGTAATATCTATTTTACC 2109  
QY 1862 AAAGTATTTAATATTTTATGCAAACTTAGATCAACTATTTTGTAGCTTGTGAAT 1921  
Db 2110 AAAGTATTTAATATTTTATGCAAACTTAGATCAACTATTTTGTAGCTTGTGAAT 2169

QY 1922 TTTTCTAAACAAATTTGTTATAGCCAGAGGAAACAPAGATGGATATAAAATATTGTTGCC 1981  
Db 2170 TTTTCTAAACAAATTTGTTATAGCCAGAGGAAACAAAGATG---ATATAAATATTGTTGC 2226  
QY 1982 CTGGACAAAATACATGTATNTCCATCCCGGAATGCTGTAGAGTTGGATTAAACCTGCA 2041  
Db 2227 TCTGACAAAATACATGTATTT-CATTCCTGTATGCTGTAGAGTTAGATT-AATCTGCA 2284  
QY 2042 TTTTAAACAACTGAATTCGGGAANGGAANTTGGTAAGGTTGGCCAAANCCTTTTGA 2101  
Db 2285 TTTTAAACAACTGAATTT---GGAATAGAATGGTAAAGTT---GCAAAGACTTTTGA 2338  
QY 2102 TAAATAA 2108  
Db 2339 TAAATAA 2345  
RESULT 13  
AAC97404  
ID AAC97404 standard; cDNA; 2849 BP.  
XX  
AC AAC97404;  
XX  
DT 28-FEB-2001 (first entry)  
XX  
DE Human angiogenesis-associated protein PRO200 cDNA, SEQ ID NO:50.  
XX  
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
gene therapy; transgenic animal; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200053753-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 05-JAN-2000; 2000WO-US00219.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
XX  
(GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Faoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX WPI; 2001-090793/10.  
DR P-PSDB; AAB53074.  
XX  
XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -



XX PS Claim 58; Fig 21A-B; 293pp; English.

XX CC The invention relates to novel human angiogenesis-associated proteins

CC designated PRO proteins (AA853064-B53097), and to nucleic acids encoding

CC PRO proteins. The invention also relates to vectors and host cells

CC comprising a PRO nucleic acid, the recombinant production of a PRO

CC protein, PRO antibodies specific for a PRO protein, fusion proteins

CC comprising a PRO protein, agonists or antagonists of a PRO protein, and

CC compounds which inhibit the expression of a PRO gene. The invention

CC additionally encompasses methods of identifying modulators of PRO

CC expression or activity; diagnosing a cardiovascular, endothelial or

CC angiogenic disorder, or a susceptibility to such a disorder by detecting

CC mutations in a PRO gene, or the expression level of a PRO gene within a

CC particular tissue; treating a cardiovascular, endothelial or angiogenic

CC disorder via the administration of a PRO protein, PRO nucleic acid, or

CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a

CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial

CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the

CC administration of a PRO protein, or an agonist or antagonist thereof.

CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO

CC agonists and PRO antagonists may be used as therapeutic agents to treat

CC cardiovascular, endothelial or angiogenic disorders, such as

CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,

CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,

CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's

CC disease, or stroke. PRO nucleic acids are additionally useful in the

CC recombinant production of PRO proteins, as hybridisation probes to

CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,

CC to map genes encoding PRO proteins, to analyse genetic disorders, and in

CC gene therapy. PRO nucleic acids can also be used to produce transgenic

CC animals useful for the development and screening of potential

CC therapeutic agents. The present sequence represents a cDNA encoding a PRO

CC protein of the invention.

XX SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 93.9%; Score 1979.4; DB 22; Length 2849;

Best Local Similarity 97.7%; Pred. No. 0;

Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCGCGGTGAGTCTCACCCTCAGTCAGCCAAATGAGCTCTTCGGGCTTCCTCG 61

DB 250 CCGCGGTGAGTCTCACCCTCAGTCAGCCAAATGAGCTCTTCGGGCTTCCTCG 309

QY 62 TGACATCTGCCCTGGCGGCGAGACGAGGACTCAGCGGGAATCAACCTGAGTAGTA 121

DB 310 TGACATCTGCCCTGGCGGCGAGACGAGGACTCAGCGGGAATCAACCTGAGTAGTA 369

QY 122 AATTCAGTTTTCAGCAACAGGACAGACGAGTACAGATCTCTCAGCATGAGAGAA 181

DB 370 AATTCAGTTTTCAGCAACAGGACAGACGAGTACAGATCTCTCAGCATGAGAGAA 429

QY 182 TTATTACTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCTACTATTCCAA 241

DB 430 TTATTACTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCTACTATTCCAA 489

QY 242 GAAATACGGTCTTGGTATGAGATAGTACGATGAGGAAATGATGATGATCAACTTA 301

DB 490 GAAATACGGTCTTGGTATGAGATAGTACGATGAGGAAATGATGATGATCAACTTA 549

QY 302 CGTTTGATGAAGATTGGGCTTGAGACCCAGAGATGACATATGCAAGTATGATTTTG 361

DB 550 CGTTTGATGAAGATTGGGCTTGAGACCCAGAGATGACATATGCAAGTATGATTTTG 609

QY 362 TAGAAGTTGAGAACCCAGTATGAACTATATTAGGGCGCTGGTGGTCTTGGTACTG 421

DB 610 TAGAAGTTGAGAACCCAGTATGAACTATATTAGGGCGCTGGTGGTCTTGGTACTG 669

QY 422 TACCAGGAACAGATTCTTAAGGAATCAAAATTAGGATGAAGATTGTATCTGATGAAT 481

DB 670 TACCAGGAACAGATTCTTAAGGAATCAAAATTAGGATGAAGATTGTATCTGATGAAT 729

QY 482 ATTTTCCTTCTGAACACAGGGTTCGTGATCCACTCAACATTGTCTCATGCCAATTCACAG 541

DB 730 ATTTTCCTTCTGAACACAGGGTTCGTGATCCACTCAACATTGTCTCATGCCAATTCACAG 789

QY 542 AAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCCACTGGAACTGCTTAATATG 601

DB 750 AAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCCACTGGAACTGCTTAATATG 849

QY 602 CTATTAACCTGCTTTAGTACCTTTGAAGACCTTATTCGATATCTTGAACACAGAGATGGC 661

DB 850 CTATTAACCTGCTTTAGTACCTTTGAAGACCTTATTCGATATCTTGAACACAGAGATGGC 909

QY 662 AGTTGGACTTAGAAGATCTATATAGGCCAACTTCGGCAACTTCTTGGCAAGGCTTTTGT 721

DB 910 AGTTGGACTTAGAAGATCTATATAGGCCAACTTTGGCAACTTCTTGGCAAGGCTTTTGT 969

QY 722 TTGAAGAAAAATCAGAGTGTGATCTGAACCTTCTTAACAGAGAGAGTAAAGATTATACA 781

DB 970 TTGAAGAAAAATCAGAGTGTGATCTGAACCTTCTTAACAGAGAGAGTAAAGATTATACA 1029

QY 782 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAGAACTAAAGAGAACCGATACCA 841

DB 1030 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAGAACTAAAGAGAACCGATACCA 1089

QY 842 TTTTCTGCCAGGTTGTCTCCTGTTAAACGCTGTGGTGGAACTGTGCTGTTGTCTCC 901

DB 1090 TTTTCTGCCAGGTTGTCTCCTGTTAAACGCTGTGGTGGAACTGTGCTGTTGTCTCC 1149

QY 902 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAGTTACTTAAAAATACACAGGCTCC 961

DB 1150 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAGTTACTTAAAAATACACAGGCTCC 1209

QY 962 TTCAGTTCAGACCAAGAACCGGTGTGAGGGGATTTGCAAAATCACTACCCAGCTGGGCC 1021

DB 1210 TTCAGTTCAGACCAAGAACCGGTGTGAGGGGATTTGCAAAATCACTACCCAGCTGGGCC 1269

QY 1022 TGGAGACCATGAGAGTGTGACTGTGTGCAAGGGAGACAGAGAGATAGCGGCATC 1081

DB 1270 TGGAGACCATGAGAGTGTGACTGTGTGCAAGGGAGACAGAGAGATAGCGGCATC 1329

QY 1082 ACCACACAGAGCTCTTCCAGAGCTGTGAGTGTGCAAGGGAGACAGAGAGATAGCGGCATC 1141

DB 1330 ACCACACAGAGCTCTTCCAGAGCTGTGAGTGTGCAAGGGAGACAGAGAGATAGCGGCATC 1389

QY 1142 ATGCGTTATCTCCATCTTAAATCTCAGTGTGTTTGGTTCGAAGGACCTTTTCATCTTCAGGAT 1201

DB 1390 ATGCGTTATCTCCATCTTAAATCTCAGTGTGTTTGGTTCGAAGGACCTTTTCATCTTCAGGAT 1449

QY 1202 TTACAGTGCATCTGAAAGAGAGACATCAAAACAGAAATTAGAGTTGTGCAACAGCTCTT 1261

DB 1450 TTACAGTGCATCTGAAAGAGAGACATCAAAACAGAAATTAGAGTTGTGCAACAGCTCTT 1509

QY 1262 TTGAGAGAGGCTTAAAGGACAGAGAAAGAGTCTTCAATCGTGAAGAAAGAAATTAATG 1321

DB 1510 TTGAGAGAGGCTTAAAGGACAGAGAAAGAGTCTTCAATCGTGAAGAAAGAAATTAATG 1569

QY 1322 TTGTAATTAATAGATCAACAGCTAGTTTCAGAGTTACCATGTACATATTCACATAGCTGG 1381

DB 1570 TTGTAATTAATAGATCAACAGCTAGTTTCAGAGTTACCATGTACATATTCACATAGCTGG 1629

QY 1382 GTTCTGTATTTTCAGTTCCTTTCGATACGGCTTAGGGTATGTGCTACAGGAAAGAAACTG 1441

DB 1630 GTTCTGTATTTTCAGTTCCTTTCGATACGGCTTAGGGTATGTGCTACAGGAAAGAAACTG 1689

QY 1442 TGCAGTGAACACCTGATTCGGTTGCTTAACTTAACTTAAAGCTCCATGCTCTGGGCT 1501

DB 1690 TGCAGTGAACACCTGATTCGGTTGCTTAACTTAACTTAAAGCTCCATGCTCTGGGCT 1749

QY 1502 AAAATCGTATTAATCTGGATTTTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATAACC 1561

DB 1750 AAAATCGTATTAATCTGGATTTTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATAACC 1809

QY 1562 AGAATCTCTATGACTACAAACCTGGTTTTTTTTAAAAAGGAACATATGTTGCTATGAATTA 1621



PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 18-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 05-JUN-2001; 2001US-0874503.  
 PR 14-JUN-2001; 2001US-0882636.  
 PR 19-JUN-2001; 2001US-0886342.  
 PR 21-JUN-2001; 2001US-0887879.  
 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.  
 PA (GETH ) GENENTECH INC.  
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI; 2003-332040/31.  
 DR P-PSDB; ABU66712.  
 XX  
 PT New secreted and transmembrane PRO nucleic acids, useful for gene  
 PT therapy, in chromosome and gene mapping, as chromosome markers, in  
 PT tissue typing, and in chromosome identification -  
 XX  
 PS Claim 2; Fig 285; 660pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The  
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for  
 CC linking bioactive molecules to cells expressing PRO polypeptides,  
 CC for modulating biological activities of cells expressing PRO  
 CC polypeptides, and for identifying agonists or antagonists.  
 CC The PRO polypeptides are useful for stimulating the release of  
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating  
 CC the proliferation or differentiation of chondrocytes, and detecting the  
 CC presence of tumours. The polynucleotide sequences encoding PRO  
 CC polypeptides are useful as hybridisation probes, in chromosome and  
 CC gene mapping, in the generation of antisense RNA and DNA, in the  
 CC preparation of PRO polypeptides, for generating transgenic animals or  
 CC knockout animals, for the genetic analysis of individuals with genetic  
 CC disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs  
 CC encoding the human PRO polypeptides of the invention.  
 CC Note: The sequence data for this patent was obtained in electronic  
 CC format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipsd/entry.html.  
 XX  
 SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;  
 Query Match 93.9%; Score 1979.4; DB 25; Length 2849;  
 Best Local Similarity 97.7%; Pred. No. 0;  
 Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;  
 QY 2 CCGCCCGTGAAGTGAAGCTCTCACCCAGTACAGGGAATGAGCCCTCTTGGGCTTCTCTGG 61  
 DB 250 CCGCCCGTGAAGTGAAGCTCTCACCCAGTACAGGGAATGAGCCCTCTTGGGCTTCTCTGC 309  
 QY 62 TGACATCTGCCCTGCCCGCAGAGAGGAGCTCAGCGGGAATCCACCTCAGTAGTA 121  
 DB 310 TGACATCTGCCCTGCCCGCAGAGAGGAGCTCAGCGGGAATCCACCTCAGTAGTA 369  
 QY 122 AATTCCAGTTTTCCAGCAACAAGGAACAGAACCGAGTACAGATCTCTCAGCATGAGAGAA 181  
 DB 370 AATTCCAGTTTTCCAGCAACAAGGAACAGAACCGAGTACAGATCTCTCAGCATGAGAGAA 429  
 QY 182 TTATTACTGTGCTTACTAATGAAGATTTTACAGCCCAAGGTTTCTCTACTATTATCCAA 241

DB 430 TTATTACTGTGCTTACTAATGAAGATTTACAGCCCAAGGTTTCTCTACTATTATCCAA 489  
 QY 242 GAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA 301  
 DB 490 GAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA 549  
 QY 302 CGTTTGATGAAGATTTGGGCTTCGAAGACCAGAGATGACATATGCAAGTATCATTTTG 361  
 DB 550 CGTTTGATGAAGATTTGGGCTTCGAAGACCAGAGATGACATATGCAAGTATCATTTTG 609  
 QY 362 TAGAAGTTGAGAAACCCAGTATGAACTATATTAGGCGCTGTGTGGTTCTCGTACTG 421  
 DB 610 TAGAAGTTGAGAAACCCAGTATGAACTATATTAGGCGCTGTGTGGTTCTCGTACTG 669  
 QY 422 TACCAGGAAACAGATTTCTAAGGGAATCAAAATTAGATAGATTTGTATCTCATGAAT 481  
 DB 670 TACCAGGAAACAGATTTCTAAGGGAATCAAAATTAGATAGATTTGTATCTCATGAAT 729  
 QY 482 ATTTTCTCTGAAACCCAGGTTCTGCATCCACTACCAATTTGTCTCATGCCAATTCACAG 541  
 DB 730 ATTTTCTCTGAAACCCAGGTTCTGCATCCACTACCAATTTGTCTCATGCCAATTCACAG 789  
 QY 542 AAGCTGTGAGTCTTTCAGTGTACCCCTTCAGCTTTGCCACTGCACTGCTGTTAATG 601  
 DB 790 AAGCTGTGAGTCTTTCAGTGTACCCCTTCAGCTTTGCCACTGCACTGCTGTTAATG 849  
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 DB 850 CTATAACTGCCCTTTAGTACCTTTGGAAGACCTTATTTCGATATCTTGAACAGAGATGGC 909  
 QY 662 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGT 721  
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 QY 722 TTGGAGAAATCCAGTGTGTGATCTGACCTTCTAACAGAGAGGTAGATATACA 781  
 DB 970 TTGGAGAAATCCAGTGTGTGATCTGACCTTCTAACAGAGAGGTAGATATACA 1029  
 QY 782 GGTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACA 841  
 DB 1030 GGTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACA 1089  
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 DB 1090 TTTTCTGGCCAGGTTGTCTCTGTTAAACGCTGTGTGGAACTGTGCTCTGTGTCTCC 1149  
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 DB 1150 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCAAGAGTCC 1209  
 QY 962 TTCAGTTGAGACCAAAAGACCGGTGTGAGGAGTGCACAAATCACTACCGAGTGGGCC 1021  
 DB 1210 TTCAGTTGAGACCAAAAGACCGGTGTGAGGAGTGCACAAATCACTACCGAGTGGGCC 1269  
 QY 1022 TCGAGCACCATGAGAGGTGTGACTGTGTGTCAGAGGAGCAGCAGAGAGATAGCCGATC 1081  
 DB 1270 TCGAGCACCATGAGAGGTGTGACTGTGTGTCAGAGGAGCAGCAGAGAGATAGCCGATC 1329  
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 DB 1330 ACCACACAGCAGCTTTCGCCAGAGCTGTGCAAGTGCAGTGGCTGATTTCTATTAGAGAACGT 1389  
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 DB 1390 ATGCGTTATCTCCATCTTAATCTCAGTTGTTCTCTCAGGAGCTTCTCATCTTCAGGAT 1449  
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 QY 1262 TTGAGAGAGGCTTAAAGGACAGGAGAAAGGCTTCTCAATCGTGGAAAGAAAATTAATG 1321  
 DB 1510 TTGAGAGAGGCTTAAAGGACAGGAGAAAGGCTTCTCAATCGTGGAAAGAAAATTAATG 1569

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Db 1570 TTGATTAAATAGATACCCAGCTAGTTTCAGAGTACCATGTACGTTATCCACTAGCTGG 1629
QY 1382 GTTCTGTATTTTCAGTCTTTTCGATACGGCTTAGGTAATGTCAGTACAGGAAAAAACTG 1441
Db 1630 GTTCTGTATTTTCAGTCTTTTCGATACGGCTTAGGTAATGTCAGTACAGGAAAAAACTG 1689
QY 1442 TGCAGTGCAGCACCTGATTCCTGTTGCCCTTGCTTAACCTTAAAGCTCCATGCTCCTGGCCCT 1501
Db 1690 TGCAGTGCAGCACCTGATTCCTGTTGCCCTTGCTTAACCTTAAAGCTCCATGCTCCTGGCCCT 1749
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Db 1750 AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTGGCTCATATTCACATATGTAAC 1809
QY 1562 AGACATCTTATGTACTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATGAATTA 1621
Db 1810 AGACATCTTATGTACTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATGAATTA 1669
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QY 1682 ATTTAGAGAGAGAGAACTACATTCATGTTTGGAGAGATATAAACCCTGAAAGAGAGTGG 1741
Db 1930 ATTTAGAGAGAGAGAACTACATTCATGTTTGGAGAGATATAAACCCTGAAAGAGAGTGG 1989
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Db 2050 CTCCTTTTGACATTAATCTGTTGCTTTTCTATCTGTTTAAATATATCTATTTTACC 2109
QY 1862 AAAGTATTTAATATCTTTTATGACAACTTAGATCAACTATTTTATGCTTGGTAAAT 1921
Db 2110 AAAGTATTTAATATCTTTTATGACAACTTAGATCAACTATTTTATGCTTGGTAAAT 2169
QY 1922 TTTTCTAAACAAATGTTATAGCCAGGAGCAAGATGATATAAATATTTGTTGCC 1981
Db 2170 TTTTCTAAACAAATGTTATAGCCAGGAGCAAGATG---ATATAAATATTTGTTGCC 2226
QY 1982 CTGGACAAAATACATGATTTTCCATCCCGAATGGTCTAGAGTTGGATTAAACCTGCA 2041
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QY 2042 TTTTAAACAACTGATTTGGGANGAANTTGGTAAAGTTGGCCCAACCTTTTGGAAA 2101
Db 2285 TTTTAAACAACTGATTT---GGAATAGAATTGGTAAAGTT---GCAAGAACTTTTGGAAA 2338
QY 2102 TAAATTA 2108
Db 2339 TAAATTA 2345

RESULT 15
ID ACA04166
XX ACA04166;
AC ACA04166;
XX
DT 27-MAY-2003 (first entry)
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 285.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defects; premature aging; AIDS; biosensor;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW bioindicator; tumour.
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PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 23-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 22-JUN-2001; 2001WO-US20116.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 18-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 14-JUN-2001; 2001US-0866034.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 05-JUN-2001; 2001US-0874503.  
 PR 14-JUN-2001; 2001US-0882636.  
 PR 19-JUN-2001; 2001US-0886342.  
 PR 21-JUN-2001; 2001US-0887879.  
 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.  
 XX  
 PA (SETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI: 2003-331925/31.  
 P-PSDB: ABU66988.  
 XX  
 FT New secreted and transmembrane nucleic acids and polypeptides,  
 FT designated as PRO, useful for treating inflammation, organ failure,  
 FT atherosclerosis, cardiac injury, infertility, birth defects, premature  
 FT aging, AIDS, or cancer  
 PS  
 Claim 2; Fig 285; 659pp; English.

XX The invention relates to an isolated nucleic acid comprising, or which is  
 CC at least 80% identical to, or the full-length coding sequence of, any of  
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide  
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid  
 CC further comprises the full-length coding sequence of the DNA deposited  
 CC under American Type Culture Collection (ATCC) accession number in a list  
 CC given in the specification. Also included are vectors and host  
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO  
 CC antibodies, PRO extracellular domains and mature sequences, methods  
 CC of detecting PRO proteins, methods for stimulating the release of  
 CC TNF-alpha (tumor necrosis factor alpha) from human blood,  
 CC (and the proliferation of differentiation of chondrocyte cells, the  
 CC proliferation of, or gene expression in pericyte cells, the release or  
 CC proteoglycans from cartilage, proliferation of inner ear articular  
 CC supporting cells, the proliferation of T-lymphocyte cells, the release  
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the  
 CC proliferation of endothelial cells), a method for modulating the uptake  
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,  
 CC a method for inhibiting the binding of A-peptide to factor VIIA,  
 CC or the differentiation of adipocyte cells, a method for detecting the  
 CC presence of a tumour in a mammal and an oligonucleotide probe derived

CC from any of the nucleotide sequences cited above. The nucleic acids and  
 CC polypeptides are useful for treating inflammatory diseases, organ  
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,  
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or  
 CC diabetic complications. The nucleic acids are useful as hybridisation  
 CC probes, in chromosome and gene mapping, and in generating antisense RNA  
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors. Both are useful in tissue typing.  
 CC The present sequence encodes a PRO protein of the invention.

XX Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 93.9%; Score 1979.4; DB 25; Length 2849;

Best Local Similarity 97.7%; Pred. No. 0;

Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCGCCGTTGAGTGAGCTCTCACCCAGTCAAGCAAAATGAGCCTCTTGGGCTTCTCTGG 61  
 DB 250 CCGCCGTTGAGTGAGCTCTCACCCAGTCAAGCAAAATGAGCCTCTTGGGCTTCTCTGG 309  
 QY 62 TGACATCTGCCTGCGCGCCGAGAGACGAGGAGCTCAGCGCGAATCCAACTGAGTAGTA 121  
 DB 310 TGACATCTGCCTGCGCGCCGAGAGACGAGGAGCTCAGCGCGAATCCAACTGAGTAGTA 369  
 QY 122 AATCCAGTTTTCAGCAACCAAGGAACAGAACGAGATCAAGATCCTCAGCATGAGAGAA 181  
 DB 370 AATCCAGTTTTCAGCAACCAAGGAACAGAACGAGATCAAGATCCTCAGCATGAGAGAA 429  
 QY 182 TTATTACTGTCTACTAATCGAAGTATTCACGCCCAAGGTTTCTCATACTTATCCAA 241  
 DB 430 TTATTACTGTCTACTAATCGAAGTATTCACGCCCAAGGTTTCTCATACTTATCCAA 489  
 QY 242 GAAATACCGTCTTGGTATGAGATTTAGTAGCAGTAGAGAGAAATGTATGATACAACTTA 301  
 DB 490 GAAATACCGTCTTGGTATGAGATTTAGTAGCAGTAGAGAGAAATGTATGATACAACTTA 549  
 QY 302 CGTTTGATGAAGATTTGGGCTTGAAGACCAGAGATGACATATGCAAGTATGATTTG 361  
 DB 550 CGTTTGATGAAGATTTGGGCTTGAAGACCAGAGATGACATATGCAAGTATGATTTG 609  
 QY 362 TAGAAGTTGAGAACCCAGTCATGGAACATATATTAGGGCGCTGGTGTGTTCTGGTACTG 421  
 DB 610 TAGAAGTTGAGAACCCAGTCATGGAACATATATTAGGGCGCTGGTGTGTTCTGGTACTG 669  
 QY 422 TACAGGAAAAACAGATTTCTAAAGAAATCAAAATTAGGATTAAGATTTGATCTGATGAAT 481  
 DB 670 TACAGGAAAAACAGATTTCTAAAGAAATCAAAATTAGGATTAAGATTTGATCTGATGAAT 729  
 QY 482 ATTTTCTTCTGAAACCGGGTTCTGCATCCACTCAACATTTGTCATGCCAAATTCACAG 541  
 DB 730 ATTTTCTTCTGAAACCGGGTTCTGCATCCACTCAACATTTGTCATGCCAAATTCACAG 789  
 QY 542 AAGCTGTGAGTCTTCTAGTGTACCCCTTCCAGCTTTGCCACTGCACTGGCTTAAATATG 601  
 DB 790 AAGCTGTGAGTCTTCTAGTGTACCCCTTCCAGCTTTGCCACTGCACTGGCTTAAATATG 849  
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 QY 662 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGT 721  
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QY 1262 TTGAGAGGAGGCTTAAAGGACAGAGAAAGGCTCTCAATCGTGGAAAGAAATTAATG 1321  
Db 1510 TTGAGAGGAGGCTTAAAGGACAGAGAAAGGCTCTCAATCGTGGAAAGAAATTAATG 1569  
QY 1322 TTGTAATTAATAGATCACAGCTAGTTTCAGAGTTACAGTACGATTCAGTATTCAGTGTG 1381  
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Db 1870 ACTTGTGTCGTGATAGGACAGCTGATTTTCTATTTTCTATTTTCTATTTTCTATTTTCTG 1929  
QY 1682 ATTTAGAGAGAGAACTACATTCATGTTTGGAGAGATAAACCTGAAAGAGAGAGTGG 1741  
Db 1930 ATTTAGAGAGAGAACTACATTCATGTTTGGAGAGATAAACCTGAAAGAGAGAGTGG 1989  
QY 1742 CCTTATCTTCACTTATCGATAAGTCACTTTATTTGTTTCACTTGTGTGATCACTTTTATAT 1801  
Db 1990 CCTTATCTTCACTTATCGATAAGTCACTTTATTTGTTTCACTTGTGTGATCACTTTTATAT 2049  
QY 1802 CTCCTTTTGACATTAATCTGCTTTTCTTAATCTTTGTTAAATATATCTATTTTCTAC 1861  
Db 2050 CTCCTTTTGACATTAATCTGCTTTTCTTAATCTTTGTTAAATATATCTATTTTCTAC 2109  
QY 1862 AAAGGTATTTAATATCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGTAAAT 1921  
Db 2110 AAAGGTATTTAATATCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGTAAAT 2169  
QY 1922 TTTTCTAAACAAATTTGTATAGCCAGAGGACAAAGATGGATATAAATAATTTGTTGCC 1981

Db 2170 TTTTCTAAACAAATTTGTATAGCCAGAGGACAAAGATG---ATATAAAATATTGTTGC 2226  
QY 1982 CTGGACAAAAATACATGTATNTCCATCCCGGAATGGTGTAGAGTTGGATTAAACCTGCA 2041  
Db 2227 TCTGACAAAAATACATGTATTT---CATTCCTGTATGCTAGAGTTAGATT---AATCTGCA 2284  
QY 2042 TTTTAAAAAACCTGAATTTGGGAANGGAANTTGGTAAGTTGGCCAAANCTTTTTTTGAAAA 2101  
Db 2285 TTTTAAAAAACCTGAATTT---GGATAGATTTGGTAAGTT---GCAAGACCTTTTGGAAAA 2338  
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GenCore version 5.1.6  
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Title: US-09-852-209A-2

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Maximum Match 100%

**Listing first 45 summaries**

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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		Match	%				
1	1979.4	93.9	2825	4	US-09-040-220D-1		Sequence 1, Appli
2	1979.4	93.9	2825	4	US-09-265-686-1		Sequence 1, Appli
3	1624.8	77.1	1760	4	US-09-584-95D-32		Sequence 32, Appli
4	1624.8	77.1	1760	4	US-09-706-968-1		Sequence 1, Appli
5	1610.8	76.4	1764	4	US-09-457-066-1		Sequence 1, Appli
6	994.8	47.2	1095	4	US-09-457-066-50		Sequence 50, Appli
7	994.8	47.2	1095	4	US-09-706-968-50		Sequence 50, Appli
8	959.4	45.5	3571	4	US-09-584-95D-34		Sequence 34, Appli
9	959.4	45.5	3571	4	US-09-706-968-42		Sequence 42, Appli
10	958.4	45.5	3573	4	US-09-457-066-42		Sequence 42, Appli
11	734.4	34.8	1035	4	US-09-457-066-6		Sequence 6, Appli
12	734.4	34.8	1035	4	US-09-706-968-6		Sequence 6, Appli
13	177.6	8.4	1110	4	US-09-584-95D-6		Sequence 6, Appli
14	117.8	5.6	1472	4	US-09-540-224-3		Sequence 3, Appli
15	117.8	5.6	1472	4	US-09-584-95D-52		Sequence 52, Appli
16	104	4.9	1882	4	US-09-540-224-1		Sequence 1, Appli
17	104	4.9	1882	4	US-09-584-95D-1		Sequence 1, Appli
18	104	4.9	1882	4	US-09-706-968-36		Sequence 36, Appli
19	102.8	4.9	1910	4	US-09-457-066-36		Sequence 36, Appli
20	55.2	2.6	6243	2	US-09-036-075-1		Sequence 1, Appli
21	52.2	2.5	19124	2	US-08-487-826B-13		Sequence 13, Appli
22	50.4	2.4	837	3	US-08-998-416-288		Sequence 288, App
23	50	2.4	2846	4	US-09-996-243-230		Sequence 230, App
24	50	2.4	19124	2	US-08-487-826B-13		Sequence 13, Appli
25	49.2	2.3	636	3	US-08-998-416-1137		Sequence 1137, App
26	48.8	2.3	1342	4	US-09-489-847-89		Sequence 89, Appli
27	47.8	2.3	1664976	4	US-08-916-421B-1		Sequence 1, Appli

C 28	46.6	2.2	10640	4	US-09-417-485D-5	Sequence 5, Appl
C 29	46.2	2.2	8920	2	US-08-446-855A-1	Sequence 1, Appl
C 30	46.2	2.2	8920	3	US-09-150-741-1	Sequence 1, Appl
C 31	45.8	2.2	4185	4	US-09-417-485D-7	Sequence 7, Appl
C 32	45.4	2.2	2450	1	US-08-628-417-6	Sequence 6, Appl
C 33	45.4	2.2	1641	1	US-08-300-903A-8	Sequence 8, Appl
C 34	45.4	2.2	1641	4	US-08-988-197-8	Sequence 8, Appl
C 35	44	2.1	2434	4	US-09-489-847-67	Sequence 67, Appl
C 36	44	2.1	2447	2	US-09-014-969-14	Sequence 14, Appl
C 37	43.8	2.1	3275	4	US-08-370-838-151	Sequence 151, App
C 38	43.6	2.1	5178	4	US-08-602-877A-95	Sequence 95, Appl
C 39	43.4	2.1	10640	4	US-09-417-485D-5	Sequence 5, Appl
C 40	43	2.0	51952	3	US-08-947-823-1	Sequence 1, Appl
C 41	42.8	2.0	854	3	US-08-998-416-534	Sequence 534, App
C 42	42.8	2.0	860	3	US-08-998-416-287	Sequence 287, Appl
C 43	42.8	2.0	1696	4	US-09-835-811-1	Sequence 1, Appl
C 44	42.8	2.0	53332	2	US-09-801-861-3	Sequence 3, Appl
C 45	42.4	2.0	663	3	US-08-998-416-191	Sequence 191, App

## ALIGNMENTS

## RESULT 1

```

US-09-040-220D-1
; Sequence 1, Application US/09040220D
; Patent No. 6391311
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HO
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACI
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACID
; TITLE OF INVENTION: AND PROCESSES FOR THEIR PR
; FILE REFERENCE: P1122
; CURRENT APPLICATION NUMBER: US/09/040,220D
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 1
; LENGTH: 2825
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: Human
; LOCATION: 2689
; OTHER INFORMATION: N is A, T, C or G
US-09-040-220D-1

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Query Match	93.9%;	Score 1979.4;	DB 4;	Length 2825;
Best Local Similarity	97.7%;	Pred. No. 0;		
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QY	2	CCCGCGGTGAGTCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCCTCGG	61	
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QY	62	TGACATCTGCCCTGGCCGCGCAGACGAGGGGACTCAGCGGAAATCCAACTTGAGTAGTA	121	
DB	284	TGACATCTGCCCTGGCCGCGCAGACGAGGGGACTCAGCGGAAATCCAACTTGAGTAGTA	343	
QY	122	AATCCAGTTTTCCAGCAACGAGGAACAGAACTGCGGATCCTCAGCATGAGAGAA	181	
DB	344	AATCCAGTTTTCCAGCAACGAGGAACAGAACTGCGGATCCTCAGCATGAGAGAA	403	
QY	182	TTATTACTGTGTCTACTAATGGAAGTATTCAAGCCCAAGGTTTCCCTCATCTTATCCAA	241	
DB	404	TTATTACTGTGTCTACTAATGGAAGTATTCAAGCCCAAGGTTTCCCTCATCTTATCCAA	463	
QY	242	GAATACCGTCTTGCTATGGAGATTAGTAGCAGTAGAGGAAATCTATGGAATACACTTA	301	
DB	464	GAATACCGTCTTGCTATGGAGATTAGTAGCAGTAGAGGAAATCTATGGAATACACTTA	523	
QY	302	CGTTTGTATGAAGATTTCGGGCTTGAAGACCCAGCAAGATGCAATATGCAAGTATGATTTTG	361	



524	Db	 CGTTTCATGAAAGATTGGCTTGAAGACCCAGAATCACATATGCAAAGTAGATGTTTTG	583
362	Qy	TAGAAGTTCAGGAACCCAGTGATGGAACATATATTAGGCGCTGGTGTGTTCTGGTACTG	421
584	Db	TAGAAGTTGAGGAACCCAGTGATGGAACATATATTAGGCGCTGGTGTGTTCTGGTACTG	643
422	Qy	TACCAGAAAACAAGATTTCTAAGAGAAATCAAATTAGGATATAGATTTGTATCTGATGAAT	481
644	Db	TACCAGAAAACAAGATTTCTAAGAGAAATCAAATTAGGATATAGATTTGTATCTGATGAAT	703
482	Qy	ATTTTCCTTCTGAACCAAGGTTCTGCATCCACTTACAAATTTGTCATGCCACAATTCACAG	541
704	Db	ATTTTCCTTCTGAACCAAGGTTCTGCATCCACTTACAAATTTGTCATGCCACAATTCACAG	763
542	Qy	AAGCTGTGAGTCTTTCAGTGTACCCCCTTTCAGCTTTGCCACTGGACCTGCTTAATAATG	601
764	Db	NAGCTGTGAGTCTTTCAGTGTACCCCCTTTCAGCTTTGCCACTGGACCTGCTTAATAATG	823
602	Qy	CTATAACTGCCTTTAGTACTTTGGAGACCTTATTCGATATCTTTGAACAGAGAGATGCC	661
824	Db	CTATAACTGCCTTTAGTACTTTGGAGACCTTATTCGATATCTTTGAACAGAGAGATGCC	883
662	Qy	AGTTGGACTTTAGAAGATCTATATAGGCCAACCTTGGCAACTCTTTGGCAAGGCTTTTGT	721
884	Db	AGTTGGACTTTAGAAGATCTATATAGGCCAACCTTGGCAACTCTTTGGCAAGGCTTTTGT	943
722	Qy	TTTGGAGAAANTCCAGAGTGGTGAATCTGAACCTTCTAAGAGGAGGTAAGATTATACA	781
944	Db	TTTGGAGAAANTCCAGAGTGGTGAATCTGAACCTTCTAAGAGGAGGTAAGATTATACA	1003
782	Qy	GCTGCACACCTCGTAATCTTTCAGTGTCCAATAAGGGAAGAACTTAAAGAGAACCGATACA	841
1004	Db	GCTGCACACCTCGTAATCTTTCAGTGTCCAATAAGGGAAGAACTTAAAGAGAACCGATACA	1063
842	Qy	TTTTCTGGCCAGGTTGTCTCTGGTTTAAACGCTGTGGTGGGAACTGTGCTGTGTCTCC	901
1064	Db	TTTTCTGGCCAGGTTGTCTCTGGTTTAAACGCTGTGGTGGGAACTGTGCTGTGTCTCC	1123
902	Qy	ACHAATTTGCAATGAATGTCAATGTGTCCAGCAAAAGTTTACTAAAAAATACCAAGAGTCC	961
1124	Db	ACHAATTTGCAATGAATGTCAATGTGTCCAGCAAAAGTTTACTAAAAAATACCAAGAGTCC	1183
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1544	Db	TTGTATTAAATAGATCACACGACTAGTTTTCAGAGTTACCATGTACGTTATTCACCTAGCTGG	1603
1382	Qy	GTTCCTGTATTCTCAGTTCTTTCGATACCGCTTAGGTTAATGTCTAGTACAGGAAAAAATCTG	1441

1604	DB	GTTCGTATTTTCAGTTCCTTCATACGGCTTAGGCTAATGTCAGTACAGAAAAAACAATCG	1666
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1724	DB	AAAACTGATATAAACTCGAATTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAACCC	1783
1562	QY	AGAACATTCCTATGTACTACAAACCTGGTTTTTAAAAAGGAACCTATGTCCTATGAAATTA	1621
1784	DB	AGAACATTCCTATGTACTACAAACCTGGTTTTTAAAAAGGAACCTATGTCCTATGAAATTA	1843
1622	QY	ACTTGTGTCGTCTGATAGACAGACGTGAAATTTTTCATATTTCTTATTAATAATTTCTGCC	1681
1844	DB	ACTTGTGTCGTCTGATAGACAGACGTGAAATTTTTCATATTTCTTATTAATAATTTCTGCC	1903
1682	QY	ATTTAGAAGAAGAACTACATTCATGGTTTGGAGAGATAAACCTGAAAAAGAGAGTGG	1741
1904	DB	ATTTAGAAGAAGAACTACATTCATGGTTTGGAGAGATAAACCTGAAAAAGAGAGTGG	1963
1742	QY	CCCTATCTTCACCTTATCGAATAGTCAGTTTATTTGGTTTCATTGTGTACATTTTATATTT	1801
1964	DB	CCCTATCTTCACCTTATCGAATAGTCAGTTTATTTGGTTTCATTGTGTACATTTTATATTT	2023
1802	QY	CTCCTTTTGACATTATAAAGTGTGGCTTTTCTAACTCTGTTAAATAATCTATTTTATACC	1861
2024	DB	CTCCTTTTGACATTATAAAGTGTGGCTTTTCTAACTCTGTTAAATAATCTATTTTATACC	2083
1862	QY	AAAGGTATTTAATATCTTTTTTATGACAACTAGATCAACTATTTTTTACGTGGTAAAT	1921
2084	DB	AAAGGTATTTAATATCTTTTTTATGACAACTAGATCAACTATTTTTTACGTGGTAAAT	2143
1922	QY	TTTTCTTAAACACAAATTTGTTATAGCCAGAGGAACAAAGATGGATATAAAAATATGTTGCC	1981
2144	DB	TTTTCTTAAACACAAATTTGTTATAGCCAGAGGAACAAAGATG---ATATAAATAATTTGTGC	2200
1982	QY	CTGGACAAAATAACATGTATNTCCATCCCGGAATGCTGTAGAGTTGGATTAACACTGCA	2041
2201	DB	CTGGACAAAATAACATGTATNT---CATCTCGTATGCTGTAGAGTTAGATTTAATCTGCA	2258
2042	QY	TTTTTAAAAAACCTGGAATTCGGGANGGAANTTGTTAAGGTTGGCCAAANCTTTTTTCAAAA	2101
2259	DB	TTTTTAAAAAACCTGGAATTT---GGAAATAGAATTTGGTAAGTT---GCAAAAGACTTTTGAAAA	2312
2102	QY	TAATTTAA 2108	
2313	DB	TAATTTAA 2319	

RESULT 2  
US-09-265-686-1  
; Sequence 1, Application US/09265686  
; Patent No. 6455283  
; GENERAL INFORMATION:  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Kuo, Sophia S.  
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1  
; FILE REFERENCE: P1122P2  
; CURRENT APPLICATION NUMBER: US/09/265,686  
; CURRENT FILING DATE: 1999-03-10  
; PRIOR APPLICATION NUMBER: US 09/040,220  
; PRIOR FILING DATE: 1998-03-17  
; PRIOR APPLICATION NUMBER: US 09/184,216  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 1  
; LENGTH: 2825  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: Unknown

; LOCATION: 2689									
; OTHER INFORMATION: Any nucleotide									
US-09-265-686-1									
Query Match		93.9%	Score	1979.4	DB 4	Length	2825		
Best Local Similarity		97.7%	Pred. No.	0					
Matches 2059		Conservative	1	Mismatches	36	Indels	11	Gaps	5
QY	2	CCGCGCGTGTAGTGAGTCTCTACCCAGTCAAGCAAAATGAGCCCTCTTCGGGCTCTCTCCTGG	61						
DB	224	CCGCGCGTGTAGTGAGTCTCTACCCAGTCAAGCAAAATGAGCCCTCTTCGGGCTCTCTCCTGC	283						
QY	62	TGACATCTGCCCTGGCGCGGCAGAGACGAGGGACTCAGGCGGAATCCAACTCAGTAGTA	121						
DB	284	TGACATCTGCCCTGGCGCGGCAGAGACGAGGGACTCAGGCGGAATCCAACTCAGTAGTA	343						
QY	122	AAATTCAGTTTTTCCAGCAACAAAGAAACAGAAACGAGTACAAGATCTCTCAGCATGAGAGAA	181						
DB	344	AAATTCAGTTTTTCCAGCAACAAAGAAACAGAAACGAGTACAAGATCTCTCAGCATGAGAGAA	403						
QY	182	TTATTAATCTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATCTTATCCAA	241						
DB	404	TTATTAATCTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATCTTATCCAA	463						
QY	242	GAATAACGGTCTTTGGTATGAGATTTAGTACGAGTAGAGGAAATGATGATGATCAACTTA	301						
DB	464	GAATAACGGTCTTTGGTATGAGATTTAGTACGAGTAGAGGAAATGATGATGATCAACTTA	523						
QY	302	CGTTTGATGAAAGATTTGGGCTTGAGACCCAGAGATGACATATGCAAGTATGATTTTG	361						
DB	524	CGTTTGATGAAAGATTTGGGCTTGAGACCCAGAGATGACATATGCAAGTATGATTTTG	583						
QY	362	TAGAAGTTGAGGAACCCAGTGATGGAATATATTAGGCGCTGCTGTGGTTCCTGCTACTG	421						
DB	584	TAGAAGTTGAGGAACCCAGTGATGGAATATATTAGGCGCTGCTGTGGTTCCTGCTACTG	643						
QY	422	TACAGGAAACAGATTTCTAAAGGAAATCAAAATAGGATGAAGATTTGTATCTGATGAAT	481						
DB	644	TACAGGAAACAGATTTCTAAAGGAAATCAAAATAGGATGAAGATTTGTATCTGATGAAT	703						
QY	482	ATTTTCTCTTCTGAACACAGGGTTCGCAATCCACTACAACTTTGTCATGCCACAATTCACAG	541						
DB	704	ATTTTCTCTTCTGAACACAGGGTTCGCAATCCACTACAACTTTGTCATGCCACAATTCACAG	763						
QY	542	AAGCTGTAGTCTCTTCAAGTGTACCCCTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG	601						
DB	764	AAGCTGTAGTCTCTTCAAGTGTACCCCTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG	823						
QY	602	CTATAACTGCTCTTTAGTACCTTGGAGACCTTATTCGATATCTTTGAACACAGAGATGGC	661						
DB	824	CTATAACTGCTCTTTAGTACCTTGGAGACCTTATTCGATATCTTTGAACACAGAGATGGC	883						
QY	662	AGTTGGAATCTAGAGATCTATATAGGCAACTTGGCAACTCTTGGCAAGCTTTTGTGTTT	721						
DB	884	AGTTGGAATCTAGAGATCTATATAGGCAACTTGGCAACTCTTGGCAAGCTTTTGTGTTT	943						
QY	722	TTGGAAGAAATCCAGAGTGTGGATCTGAACCTTCTTAACAGAGAGGTAAATATATACA	781						
DB	944	TTGGAAGAAATCCAGAGTGTGGATCTGAACCTTCTTAACAGAGAGGTAAATATATACA	1003						
QY	782	GCTGCACACTCGTAACTCTCAGTGTCCATAAGGGGAAGAACTAAAGAGAACCGATACCA	841						
DB	1004	GCTGCACACTCGTAACTCTCAGTGTCCATAAGGGGAAGAACTAAAGAGAACCGATACCA	1063						
QY	842	TTTTTCTGGCCAGTGTGCTCCTGCTGTTAAACGCTGTGTGGGAACTGTGCTGTTGTCTCC	901						
DB	1064	TTTTTCTGGCCAGTGTGCTCCTGCTGTTAAACGCTGTGTGGGAACTGTGCTGTTGTCTCC	1123						
QY	902	ACAAATTCGAATGATGTCAATGTCTCCCAAGCAAAAGTTACTAAAAATACCAAGAGTCC	961						
DB	1124	ACAAATTCGAATGATGTCAATGTCTCCCAAGCAAAAGTTACTAAAAATACCAAGAGTCC	1183						
QY	962	TTCAAGTTGAGACCAAGACCGGTTGTACGGGATTCGACAAATCTACCCAGCGTGGCC	1021						

DB	1184	TTCAAGTTGAGACCAAGACCGGTGTACGGGATTTGCACAAATCACTACCGACGTGGCCC	1243						
QY	1022	TGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGTAGCCGATC	1081						
DB	1244	TGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGTAGCCGATC	1303						
QY	1082	ACCACAGGAGCTCTTGCAGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG	1141						
DB	1304	ACCACAGGAGCTCTTGCAGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG	1363						
QY	1142	ATGCGGTATCTCATCTTAAATCTCAGTGTGTTTGTCTTCAAGGACCTTTCATCTTCAGGAT	1201						
DB	1364	ATGCGGTATCTCATCTTAAATCTCAGTGTGTTTGTCTTCAAGGACCTTTCATCTTCAGGAT	1423						
QY	1202	TTACAGTGTATCTGAAAGAGAGACATCAAAACAGAAATAGGAGTGTGCAACAGCTCTT	1261						
DB	1424	TTACAGTGTATCTGAAAGAGAGACATCAAAACAGAAATAGGAGTGTGCAACAGCTCTT	1483						
QY	1262	TTGAGAGGAGGCTTAAAGACAGGAGAAAGTCTTCAATCGTGAAGAAATTAATG	1321						
DB	1484	TTGAGAGGAGGCTTAAAGACAGGAGAAAGTCTTCAATCGTGAAGAAATTAATG	1543						
QY	1322	TTGTATTAATAGATCACAGCTAGTTTCAGAGTTCACATGTACGTATTCACATGTG	1381						
DB	1544	TTGTATTAATAGATCACAGCTAGTTTCAGAGTTCACATGTACGTATTCACATGTG	1603						
QY	1382	GTTCTGTATTTTCAGTCTTTCGATACGGCTTAGGGTAATGTGAGTACAGGAAATAAATG	1441						
DB	1604	GTTCTGTATTTTCAGTCTTTCGATACGGCTTAGGGTAATGTGAGTACAGGAAATAAATG	1663						
QY	1442	TGCAAGTGTAGACCTGATTCGGTTCGCTTGTCTTAACTCTAAAGCTTCAATGTCTGGGCT	1501						
DB	1664	TGCAAGTGTAGACCTGATTCGGTTCGCTTGTCTTAACTCTAAAGCTTCAATGTCTGGGCT	1723						
QY	1502	AAATTCGTATTAATCTGGAATTTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1561						
DB	1724	AAATTCGTATTAATCTGGAATTTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1783						
QY	1562	AGAAATTTCTATGTACTACAAACCTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1621						
DB	1784	AGAAATTTCTATGTACTACAAACCTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1843						
QY	1622	ACTGTGCTGCTGCTGATAGGACAGACTGATTTTCTTCTTCTTCTTCTTCTTCTTCTT	1681						
DB	1844	ACTGTGCTGCTGCTGATAGGACAGACTGATTTTCTTCTTCTTCTTCTTCTTCTTCTT	1903						
QY	1682	ATTTAGAGAGAGAACTACATTCATGTTTGGAGAGATAAACCCTGAAAAGAGAGTGG	1741						
DB	1904	ATTTAGAGAGAGAACTACATTCATGTTTGGAGAGATAAACCCTGAAAAGAGAGTGG	1963						
QY	1742	CTTTATCTTCTCATCTTATCGATTAAGTCAAGTTTATTTGTTTCTTCTTCTTCTTCTT	1801						
DB	1964	CTTTATCTTCTCATCTTATCGATTAAGTCAAGTTTATTTGTTTCTTCTTCTTCTTCTT	2023						
QY	1802	CTCTTTTTCAGATTAATCTGTTGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1861						
DB	2024	CTCTTTTTCAGATTAATCTGTTGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	2083						
QY	1862	AAAGGTATTTAAATATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1921						
DB	2084	AAAGGTATTTAAATATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	2143						
QY	1922	TTTTCTTAAACAAATTTATAGCCAGAGGACAAAGATGATTAATAAATATTTGTTGCC	1981						
DB	2144	TTTTCTTAAACAAATTTATAGCCAGAGGACAAAGATGATTAATAAATATTTGTTGCC	2200						
QY	1982	CTGGACAAATAATACATGTATNTCTTCCATCCGGAATGGTCTAGAGTGGATTTAAACCTGCA	2041						
DB	2201	CTGGACAAATAATACATGTATNTCTTCCATCCGGAATGGTCTAGAGTGGATTTAAACCTGCA	2258						
QY	2042	TTTTTAAATAACCTGATTTGGGAAGGAATTTGGTAAAGTGGCCAAATCTTTTGTGAAA	2101						

Db 2259 TTTTAAAAAACTGAATT---GGAATAGAAITGGTAAGTT---GCAAGAGACTTTTGAAGA 2312

Qy 2102 TAAATTA 2108

Db 2313 TAAATTA 2319

RESULT 3

US-09-564-595D-32  
; Sequence 32, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/564,595D  
; CURRENT FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 1760  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (154)...(1191)  
US-09-564-595D-32

Query Match 77.1%; Score 1624.8; DB 4; Length 1760;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1637; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 2 CCCGCCGTGAGTGGCTCTCACCCAGTCAGCCAAATGAGCTCTTCGGGCTTCCTCTGG 61  
Db 119 CCCGCCGTGAGTGGCTCTCACCCAGTCAGCCAAATGAGCTCTTCGGGCTTCCTCTGG 178  
Qy 62 TGACATCTGCTGCTGCGCGCGAGACGAGGAGCTCAGCGCGAATCCAACTGAGTAGTA 121  
Db 179 TGACATCTGCTGCTGCGCGCGAGACGAGGAGCTCAGCGCGAATCCAACTGAGTAGTA 238  
Qy 122 AATTCAGTCTTCCAGCAACAGGACAGACGAGTACAGATCCCTCAGCATGAGAGAA 181  
Db 239 AATTCAGTCTTCCAGCAACAGGACAGACGAGTACAGATCCCTCAGCATGAGAGAA 298  
Qy 182 TTATTAATCTGTCTACTAATGAGATTTACAGCCCAAGGTTTCCTCATCTATCCAA 241  
Db 299 TTATTAATCTGTCTACTAATGAGATTTACAGCCCAAGGTTTCCTCATCTATCCAA 358  
Qy 242 GAAATACGCTCTTGGTATGAGATTTAGTAGAGTACAGGAGGAGGATGATGAGTACAACTTA 301  
Db 359 GAAATACGCTCTTGGTATGAGATTTAGTAGAGTACAGGAGGAGGATGATGAGTACAACTTA 418  
Qy 302 CGTTTGAATGAAGATTTGGGCTTTGAAGCCCAAGATGACATATGCAAGTATGATTTG 361  
Db 419 CGTTTGAATGAAGATTTGGGCTTTGAAGCCCAAGATGACATATGCAAGTATGATTTG 478  
Qy 362 TAGAAGTTCAGGAGCCAGTGTGAGTATATATAGGCGCTGGTGTGTTCTGGTACTG 421  
Db 479 TAGAAGTTCAGGAGCCAGTGTGAGTATATATAGGCGCTGGTGTGTTCTGGTACTG 538  
Qy 422 TACCAGGAGGAGGAGGATTTCTAAGGAGGAGGATTTCTGATGATGATGATGATGATGAT 481  
Db 539 TACCAGGAGGAGGAGGATTTCTAAGGAGGAGGATTTCTGATGATGATGATGATGATGAT 598  
Qy 482 ATTTTCTCTGACACAGGAGGTTCTGATCCACTCAACATTTGTCATGACCAAAATTCAG 541

Db 599 ATTTTCTCTGAAACCCAGGGTTCGCACTCAAACTTGTCTCATGCCAAATTCACAG 658  
Qy 542 AAGCTGTGAGTCCCTTCAGTGTACCCCTTCAGCTTTGCCACTGGACTCTTAATAATG 601  
Db 659 AAGCTGTGAGTCCCTTCAGTGTACCCCTTCAGCTTTGCCACTGGACTCTTAATAATG 718  
Qy 602 CTATAACTGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTGAACGAGAGATGCC 661  
Db 719 CTATAACTGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTGAACGAGAGATGCC 778  
Qy 662 AGTTCGACTTTAGAAGATCTATATAGGCCAACTTCGCAACTTCTTGGCAAGGCTTTGTTT 721  
Db 779 AGTTCGACTTTAGAAGATCTATATAGGCCAACTTCGCAACTTCTTGGCAAGGCTTTGTTT 838  
Qy 722 TTGGAAGAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGAGGATGAATATACA 781  
Db 839 TTGGAAGAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGAGGATGAATATACA 898  
Qy 782 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAAGAACTAAAGAGAACCGATACCA 841  
Db 899 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAAGAACTAAAGAGAACCGATACCA 958  
Qy 842 TTTTCTGCGCAGGTTGTCTCTGTTAAACCGCTGTGTGGGAACTGTGCTGTTGCTCC 901  
Db 959 TTTTCTGCGCAGGTTGTCTCTGTTAAACCGCTGTGTGGGAACTGTGCTGTTGCTCC 1018  
Qy 902 ACAATTGCAATGAATGTCAATGTCTCCCAAGCAAGTTACTAAAAAATACCACAGGCTCC 961  
Db 1019 ACAATTGCAATGAATGTCAATGTCTCCCAAGCAAGTTACTAAAAAATACCACAGGCTCC 1078  
Qy 962 TTTAGTTGAGACCAAGAGCCGCTGTGAGGGGATTCACAAATCTACCCAGCTGGGCC 1021  
Db 1079 TTTAGTTGAGACCAAGAGCCGCTGTGAGGGGATTCACAAATCTACCCAGCTGGGCC 1138  
Qy 1022 TGAGACCATCAGAGTGTGCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1081  
Db 1139 TGAGACCATCAGAGTGTGCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1198  
Qy 1082 ACCACAGCAGCTCTTGGCCAGAGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1141  
Db 1199 ACCACAGCAGCTCTTGGCCAGAGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1258  
Qy 1142 ATGCGTATCTCATCTTAACTTCAGTGTGTTGCTTCAAGGAGGAGGAGGAGGAGGAGGAGG 1201  
Db 1259 ATGCGTATCTCATCTTAACTTCAGTGTGTTGCTTCAAGGAGGAGGAGGAGGAGGAGGAGG 1318  
Qy 1202 TTACAGTGTCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1261  
Db 1319 TTACAGTGTCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1378  
Qy 1262 TTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1321  
Db 1379 TTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1438  
Qy 1322 TTGATTTAAATAGATCACCAGCTAGTTCAGAGTTCACATGTACGTATTCACAGTGTGG 1381  
Db 1439 TTGATTTAAATAGATCACCAGCTAGTTCAGAGTTCACATGTACGTATTCACAGTGTGG 1498  
Qy 1382 GTTCTGTATTTTCTGATTCGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACG 1441  
Db 1499 GTTCTGTATTTTCTGATTCGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACG 1558  
Qy 1442 TCCAGTGTAGCAGCTTGTTCGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 1501  
Db 1559 TCCAGTGTAGCAGCTTGTTCGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 1618  
Qy 1502 AAAATCGTATAAAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1560  
Db 1619 AAAATCGTATAAAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1678  
Qy 1561 CAGAACATTTCTATGTAACAACCTGGTTTTTAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1620

DB	1679	CAGAACATTCATGTACTACAAACCTGGTGTGTTTAAAAAGGAACTATGTTGCTATGAATTA	1738
QY	1621	AACTGTGTCCTGCTGATAGGA	1642
DB	1739	AACTGTGTCGTGCTGATAGGA	1760
<p>RESULT 4</p> <p>US-09-706-968-1</p> <p>; Sequence 1, Application US/09706968</p> <p>; Patent No. 6528050</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Gao, Zeren</p> <p>; APPLICANT: Hart, Charles E.</p> <p>; APPLICANT: Piddington, Christopher S.</p> <p>; APPLICANT: Sheppard, Paul O.</p> <p>; APPLICANT: Shoemaker, Kimberly E.</p> <p>; APPLICANT: Gilbertson, Debra G.</p> <p>; APPLICANT: West, James W.</p> <p>; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3</p> <p>; FILE REFERENCE: 98-60C1</p> <p>; CURRENT APPLICATION NUMBER: US/09/706,968</p> <p>; CURRENT FILING DATE: 2000-11-06</p> <p>; PRIOR APPLICATION NUMBER: US/09/541,752</p> <p>; PRIOR FILING DATE: 2000-03-31</p> <p>; NUMBER OF SEQ ID NOS: 50</p> <p>; SOFTWARE: FastSeq for Windows Version 3.0</p> <p>; SEQ ID NO 1</p> <p>; LENGTH: 1760</p> <p>; TYPE: DNA</p> <p>; ORGANISM: Homo sapiens</p> <p>; FEATURE:</p> <p>; NAME/KEY: CDS</p> <p>; LOCATION: (154)...(1191)</p> <p>US-09-706-968-1</p>			
<p>Query Match 77.1%; Score 1624.8; DB 4; Length 1760;</p> <p>Best Local Similarity 99.7%; Pred. No. 0;</p> <p>Matches 1637; Conservative 1; Mismatches 3; Indels 1; Gaps 1;</p>			
QY	2	CCCCCGGTGAGTGAGCTCTCACCCAGTCAGCCAAATAGAGCTCTTCGGGCTTCTCCTGG	61
DB	119	CCCCCGGTGAGTGAGCTCTCACCCAGTCAGCCAAATAGAGCTCTTCGGGCTTCTCCTGC	178
QY	62	TGACATCTGCCCTGGCGGCGCAGAGACGAGGAGCTCAGCGGAATCCAACTTGAGTAGTA	121
DB	179	TGACATCTGCCCTGGCGGCGCAGAGACGAGGAGCTCAGCGGAATCCAACTTGAGTAGTA	238
QY	122	AATTCAGTCTTTCAGCAACACAGGAACAGAAACGAGTACAGATCCTCAGCATCAGAGAA	181
DB	239	AATTCAGTCTTTCAGCAACACAGGAACAGAAACGAGTACAGATCCTCAGCATCAGAGAA	298
QY	182	TTATATCTGTGTCCTAATGGAAGTATTACAGCCCAAGGTTTCTCATCTTATCCAA	241
DB	299	TTATATCTGTGTCCTAATGGAAGTATTACAGCCCAAGGTTTCTCATCTTATCCAA	358
QY	242	GAATATACGGTCTTCGTATGAGATTTAGTAGCAGTAGAGAAAATGATGATACAACTTA	301
DB	359	GAATATACGGTCTTCGTATGAGATTTAGTAGCAGTAGAGAAAATGATGATACAACTTA	418
QY	302	CGTTTGATGAAGATTTGGGCTTGAGACCCAGAGATGACATATGGAAGTATGATTTTG	361
DB	419	CGTTTGATGAAGATTTGGGCTTGAGACCCAGAGATGACATATGGAAGTATGATTTTG	478
QY	362	TAGAAGTTGAGGAACCCAGTGATGGAACATAATATAGGGCGCTGGTGTGTTCTGTA	421
DB	479	TAGAAGTTGAGGAACCCAGTGATGGAACATAATATAGGGCGCTGGTGTGTTCTGTA	538
QY	422	TACACAGGAACACAGATTTCTAAGGAATCAAAATTAGGATAGATTTGATCTGATGAAT	481
DB	539	TACACAGGAACACAGATTTCTAAGGAATCAAAATTAGGATAGATTTGATCTGATGAAT	598
QY	482	ATTTTCCCTTCGAACCCAGGGTCTTGATATCCACTACAACTTGTCATGCGCAAAATTCAG	541

Db 1679 CAGAACATTCATCTACTACAAACCTGGTGTGTTTAAAAAGGAACATATGTTGCTATGAATTA 1738

Qy 1621 AACTTGTCGTCGTCGTATAGGA 1642

Db 1739 AACTTGTCGTCGTCGTATAGGA 1760

RESULT 5

US-09-457-066-1

; Sequence 1, Application US/09457066

; Patent No. 6432673

; GENERAL INFORMATION:

; APPLICANT: Gao, Zeren

; APPLICANT: Hart, Charles E.

; APPLICANT: Piddington, Christopher S.

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Shoemaker, Kimberly E.

; APPLICANT: Gilbertson, Debra G.

; APPLICANT: West, James W.

; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVSGF3

; FILE REFERENCE: 98-60

; CURRENT APPLICATION NUMBER: US/09/457,066

; CURRENT FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1760

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (154) ... (1191)

US-09-457-066-1

Query Match 76.4%; Score 1610.8; DB 4; Length 1764;

Best Local Similarity 99.5%; Pred No. 0;

Matches 1637; Conservative 1; Mismatches 3; Indels 5; Gaps 2;

Qy 2 CCCGCCGTGAGTGAGCTCTCAACCCAGTCAGCCAAATAGAGCCTCTTCGGGCTTCCTCGG 61

Db 119 CCCGCCGTGAGTGAGCTCTCAACCCAGTCAGCCAAATAGAGCCTCTTCGGGCTTCCTCGC 178

Qy 62 TCACATCTGCCCTGCCGCGCAGACGAGGAGCTCAGCGCGAATCCAACTGAGTAGTA 121

Db 179 TGACATCTGCCCTGCCGCGCAGACGAGGAGCTCAGCGCGAATCCAACTGAGTAGTA 238

Qy 122 AATTCAGGTTTCCAGCAACAGGAAACAGGAGTACAGAGTCCCTCAGCATGAGGAA 181

Db 239 AATTCAGGTTTCCAGCAACAGGAAACAGGAGTACAGAGTCCCTCAGCATGAGGAA 298

Qy 182 TTATTACTGTGTCTACTAATGGAATTTTCACAGCCCAAGGTTTCCTCATCTATCCAA 241

Db 299 TTATTACTGTGTCTACTAATGGAATTTTCACAGCCCAAGGTTTCCTCATCTATCCAA 358

Qy 242 GAAATACGGTCTTGATGAGATTTAGTAGAGTACAGGAAATAGTAGGATACAACTTA 301

Db 359 GAAATACGGTCTTGATGAGATTTAGTAGAGTACAGGAAATAGTAGGATACAACTTA 418

Qy 302 CGTTTGATGAGAAATTTGGGCTTGAAGCCAGAGATGACATATGAGGAGTATGATTTTG 361

Db 419 CGTTTGATGAGAAATTTGGGCTTGAAGCCAGAGATGACATATGAGGAGTATGATTTTG 478

Qy 362 TAGAAGTTGAGGAAACCCAGTATGGAATTTATAGGCGCTGGTGGTTCCTGTAATG 421

Db 479 TAGAAGTTGAGGAAACCCAGTATGGAATTTATAGGCGCTGGTGGTTCCTGTAATG 538

Qy 422 TACCGGAAACAGATTTCTTAAGGAATCAAAATAGGATAGATTTGATCTGATGAT 481

Db 539 TACCGGAAACAGATTTCTTAAGGAATCAAAATAGGATAGATTTGATCTGATGAT 598

Qy 482 ATTTTCCTTCTGAACACGAGGTTCTGCATCCACTACAAATTTGTCATGCGCAATTCACAG 541

Db 599 ATTTTCCTTCTGAACACGAGGTTCTGCATCCACTACAAATTTGTCATGCGCAATTCACAG 658

Qy 542 AAGCTGTGAGTCTCTCAGTGTCTACCCCTTCAGCTTTGCGCACTGAGCCTCTTAATATG 601

Db 659 AAGCTGTGAGTCTCTCAGTGTCTACCCCTTCAGCTTTGCGCACTGAGCCTCTTAATATG 718

Qy 602 CTATAACTGCGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTTGAACAGAGATGGC 661

Db 719 CTATAACTGCGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTTGAACAGAGATGGC 778

Qy 662 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTTGGCAAGCTTTTGT 721

Db 779 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTTGGCAAGCTTTTGT 838

Qy 722 TTGGAGAGAAATCCAGAGTGTGATCTGAACCTTTCTAAAGAGAGAGTAAATATATACA 781

Db 839 TTGGAGAGAAATCCAGAGTGTGATCTGAACCTTTCTAAAGAGAGAGTAAATATATACA 898

Qy 782 GCTGCACACCTCGTAACCTTCTCAGTGTCTTAAGGGAAGAACTAAAGAGAACCGATACCA 841

Db 899 GCTGCACACCTCGTAACCTTCTCAGTGTCTTAAGGGAAGAACTAAAGAGAACCGATACCA 958

Qy 842 TTTTCTGCGCAGGTTGCTCTCTGTTTAAACGCTGTGGGAACTGTGCGCTTGTCTCC 901

Db 959 TTTTCTGCGCAGGTTGCTCTCTGTTTAAACGCTGTGGGAACTGTGCGCTTGTCTCC 1018

Qy 902 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTTAAATAATACCCAGGTC 961

Db 1019 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTTAAATAATACCCAGGTC 1078

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Db 1079 TTCAGTTGAGCAAAAGACCGGTGTCAAGGAGTTGCAAAATCACTACCGAGTGGCC 1138

Qy 1022 TGGAGCACCATGAGGAGTGTCACTGTGTGCGAGGAGGAGCAGGAGGATAGCGCATC 1081

Db 1139 TGGAGCACCATGAGGAGTGTCACTGTGTGCGAGGAGGAGCAGGAGGATAGCGCATC 1198

Qy 1082 ACCACAGCAGCTCTTGGCCAGAGCTGTGAGTGTGTTTCTTCAAGGACCTTTCATCTTCA 1137

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Db 1259 AGTATGCTTATCTCCATCTTATCTCAGTGTGTTTCTTCAAGGACCTTTCATCTTCA 1318

Qy 1198 GGATTTACAGTGCATCTTGAAGAGGAGACATCAACAGAAATAGGAGTTGTGCAACAGC 1257

Db 1319 GGATTTACAGTGCATCTTGAAGAGGAGACATCAACAGAAATAGGAGTTGTGCAACAGC 1378

Qy 1258 TCTTTTGAGAGGAGGCTTAAGGAGCAGGAGAAAGGTTCTCAATCGTGAAGAAATTA 1317

Db 1379 TCTTTTGAGAGGAGGCTTAAGGAGCAGGAGAAAGGTTCTCAATCGTGAAGAAATTA 1438

Qy 1318 AATGTTGATTAATAATAGATCACAGCTAGTTTACAGGTTTACCATGATGATTTCCACTAG 1377

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Qy 1498 GCTTAAATCTGATTAATAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGT 1556

Db 1619 GCTTAAATCTGATTAATAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGT 1678

Qy 1557 AAACAGAGACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGA 1616

Db 1679 AAACAGAGACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGA 1738









1374 TAGAGTTGAGGAGCCAGTGATGGAAGTGTGTTTATGACGCTGGTGTGGTCTCGGACTG 1433  
422 TACAGGAAACAGATTTCTAAAGGAAATCAATTAGGATAGATTTGTATCTGATGAAT 481  
1434 TGGCAGGAAAGCAGACTTCTAAAGGAAATCAATCAGGATAGATTTGTATCTGATGAAT 1493  
482 ATTTCCTCTGACACCGAGGTTCTGCATCCACTACACATTTGTATGCGCACAAATCACAG 541  
1494 ATTTCCTCTGACACCGAGGTTCTGCATCCACTACACATTTGTATGCGCACAAATCACAG 1553  
542 AAGCTGTGAGTCTTCACTGCTACCCCTTCACTTTGCACTTGGACCTGCTTAATATG 601  
1554 AAACACAGAGTCTTGGTGTGGCCCTTCACTTTGTATGCGCACAAATCACAG 1613  
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1614 CTGTGACTGCTTCACTGAGTACCTTGAAGAGCTGATTCGTTACCTAGAGCCAGATGCG 1673  
662 AGTTGGACTTAGAGATCTATAGGCACTTGGCACTTGGCAAGGCTTTGTGTT 721  
1674 AGTTGGACTTAGAGATCTATAGGCACTTGGCACTTGGCAAGGCTTTGTGTT 1733  
722 TTGAAGAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGAGGTAAGATATACA 781  
1734 ATGGAAATCAAGCAAGTGTGATCTGAATCTCTCAAGGAAGAGGTAAGATATACA 1793  
782 GCTGCACACCTGTAATCTTCACTGCTCAATAGGAGGAGAACTTAAGAGAACCGATACCA 841  
1794 GCTGCACACCCGGAATCTTCACTGCTCAATAGGAGGAGAACTTAAGAGAACCGATACCA 1853  
842 TTTTCTGGCCAGGTTGTCTCTGCTTAAACGCTGTGCTGGGAACTGTGCTGTGCTCC 901  
1854 TATTTCTGGCCAGGTTGTCTCTGCTTAAACGCTGTGCTGGGAACTGTGCTGTGCTCC 1913  
902 ACAATGCAATGAATGCAATGTGCTCAAGCAAGTGTCTTAAATAATCACAGAGTCC 961  
1914 ATAATGCAATGAATGCAATGTGCTCAAGCAAGTGTCTTAAATAATCACAGAGTCC 1973  
962 TTCAGTTGAGACCAAGACCGGTTGTGAGGGAATGACAAATCACTCACGACGTCGCGC 1021  
1974 TTCAGTTGAGACCAAGACCGGTTGTGAGGGAATGACAAATCACTCACGACGTCGCGC 2033  
1022 TGGAGCACCATTAGAGAGTGTGATCTGTGTGAGGAGGAGACAGGAGGATACCGGATC 1081  
2034 TGGAGCACCATTAGAGAGTGTGATCTGTGTGAGGAGGAGACAGGAGGATACCGGATC 2093  
1082 ACCACACAGCTCTTGTCCACAGAGCTGTGAGTGTGAGTGTGATCTTATAGAGAGCT 1141  
2094 CTTGCTAGCAGACAGC-----TGAGCACTGGCAATCTGTGTACCCCAACAGCAAC 2145  
1142 ATGCTTTATCTCAATCTTAAATCTCACTGCTTGTGCTTCAAGGACCTTCACTTCAAGAT 1201  
2146 CTTATCCCAACAGAGCTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2201  
1202 TTACAGTCACTTCTGAAAGAGGAGACATCAAAAGAAATTAGAGTGTGCAACAGCTCTT 1261  
2202 AAAGATCTTATCTGCTTCAACCAATCTCACTGCTTGTGCTTCAATAGCTTCCCTGTC 2261  
1262 TTGAGAGGAGGCTTAAAGGACAGAGAAAGGCTTCAATGCTGTGGAAGAAATTAATG 1321  
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1322 TTGATTAATAGATCAACAGCTAGTTTCAAGATTTACATGTACGATTTCCACTAGCTGG 1381  
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1442 TCCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1501  
2442 TAGTTGTCTGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2501

1502 AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTAAC 1561  
2502 GATTTGTGAACAATGAGCAAA--TACTTGGATTTCTCCAACTGTTTGCATAGATAGACA 2558  
1562 AGAACATTTATGTACTACAACTGGTTTTTAAAGGAACTATCTGCTATGTAATTA 1621  
2559 GATGCTCTGTTTTCTCAAACTCAAGCTTTTAAAGGAGGAGCTATGTTAATAGGAATTA 2618  
1622 ACTTGTCTGTCTGTATGAGACAGACTGGATTTTCTATATTTCTATTTAAATTTCTGCC 1681  
2619 A--TGTCCTCTGTGAAGGAAAGAGCTGAATTTTCAA--TGCTTGGCAACTTCTCCGCA 2674  
1682 ATTTAGAGAGAGAACTACATTCATGCTGTTTGAAGAGATAAAACCTGAAAGAGAGTGG 1741  
2675 ATTTGGAGGAAAGG--TGCGGTCTGATGTTTGGAGAAAGCACACCTGCAAGAGGAGTGG 2731  
1742 CTTTATCTTCACTTTATCGATAAGTCACTTTTATTTGTTTCACTTGTGTACATTTTATATT 1801  
2732 CTTTCCCTCTGAGGTGGCTTCTGTTTCACTTGTGTATATTTTATATT 2790  
1802 CTCTTTTGAATTAATCTGTTGGCTTTCTAATCTTGTAAATATATCTATTTTATCC 1861  
2791 CTCTTTTGAATTAATCTGTTGGCTTTCTAATCTTGTAAATATATCTATTTTATCC 2850  
1862 AAAGTATTTAATATCTTTTATGACAACTTAGATCACTATTTTGTCTTGGTAA--1919  
2851 AAAGTATTTAATATCTTTTATGACAACTTAGATCACTATTTTGTCTTGGTAA--1919  
1920 -ATTTTCTTAAACAATTTGTTATAGCCAGAGGAGCAAAAGATG--GATATAAAATATT 1975  
2911 TTTTCTTAAACAATTTGTTATAGCCAGAGGAGCAAAAGATG--GATATAAAATATT 2970  
1976 GTTCCCTGAGCAAAATATGATGATTTTCCATCCGGAATGCTGCTAGAGTTCGATTA 2035  
2971 GTTCTCT-GACAAAACATATGATTTTCTTCTTGTATGCTAGAGCTTAGCGTCA 3028  
2036 CTTGCAATTTTAAAAA 2051  
3029 TCTGCAATTTGAAAGA 3044

## RESULT 10

US-09-457-066-42  
; Sequence 42, Application US/09457066  
; Patent No. 6432673

## GENERAL INFORMATION:

; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Fiddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42

; LENGTH: 3571

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1049)...(2086)

US-09-457-066-42

Query Match 45.5%; Score 958.4; DB 4; Length 3573;  
Best Local Similarity 70.5%; Pred. No. 1.2e-234;  
Matches 1450; Conservative 2; Mismatches 575; Indels 29; Gaps 12;

QY 2 CCGCCGAGTGGAGCTCTCACCCAGTCCAGCAATGAGCCTCTTCGGGCTTCTCCTGG 61  
Db 1014 CCGCCGAGTGGAGCTCTCACCCAGTCCAGCAATGAGCCTCTTCGGGCTTCTCCTGG 1073  
QY 62 TGACATCTGCGCTGGCGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 121  
Db 1074 TGACATCTGCGCTGGCGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1133  
QY 122 AATTCAGTCTTCCAGCAACAGAAACAGAAACAGAAACAGAAACAGAAACAGAAACAG 181  
Db 1134 AGTTGAGCTCTCCAGCGACAGGACAGAAACAGAAACAGAAACAGAAACAGAAACAG 1193  
QY 182 TTATTAATCTGCTTAAAGGAGTATTCAGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAG 241  
Db 1194 TTGTCATCTATCTGGTAATGGGAGCATCCAGAGCCGAGGAGGAGGAGGAGGAGGAGGAG 1253  
QY 242 GAAATACGCTCTGGTATGAGATTAAGTAGCAGTAGAGGAAATGATGGATCACTTCA 301  
Db 1254 GAAATATGGTCTGGTATGAGATTAAGTAGCAGTAGAGGAAATGATGGATCACTTCA 1313  
QY 302 GATTGATGAAGTCTGGCTTGAAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 361  
Db 1314 CATTTGATGAGATTTGGGCTGGAAGATCCAGAGCCGAGGAGGAGGAGGAGGAGGAGGAG 1373  
QY 362 TAGAAGTTGAGGAGCCAGGATGAGGAACTATATAGGGGCTGGTGTGCTTCTGGTACTG 421  
Db 1374 TAGAAGTTGAGGAGCCAGGATGAGGAACTATATAGGGGCTGGTGTGCTTCTGGTACTG 1433  
QY 422 TACAGAGAAACAGATTTCTAAAGGAAATCAAAATTAAGGATAGATTTGATCTGATGAAT 481  
Db 1434 TGCCAGGAAACAGATTTCTAAAGGAAATCAAAATTAAGGATAGATTTGATCTGATGAAT 1493  
QY 482 ATTTTCCTCTGAACAGGCTTCTGATCCACTACCAATTTGTCATGCCACAAATTCACAG 541  
Db 1494 ATTTTCCTCTGAACAGGCTTCTGATCCACTACCAATTTGTCATGCCACAAATTCACAG 1553  
QY 542 AAGCTGTGAGTCTTCAAGTCTGAGGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 601  
Db 1554 AAACACAGGCTCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1613  
QY 602 CTATACTGCTTGAACAGGCTTCTGATCCACTACCAATTTGTCATGCCACAAATTCACAG 661  
Db 1614 CTGTGAGCTGCTTGAACAGGCTTCTGATCCACTACCAATTTGTCATGCCACAAATTCACAG 1673  
QY 662 AGTTGAGCTTGAAGATCTATATAGGCAACTTGGCACTTCTTGGCAAGGCTTCTTGGT 721  
Db 1674 AGTTGAGCTTGAAGATCTATATAGGCAACTTGGCACTTCTTGGCAAGGCTTCTTGGT 1733  
QY 722 TTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTTAAAGAGGAGGTAAGATTATACA 781  
Db 1734 ATGGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTTAAAGAGGAGGTAAGATTATACA 1793  
QY 782 GCTGCACACCTGTAACTTCTGATGCTCAATAGGGAAGAACTAAAGAGAAACGATACCA 841  
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QY 842 TTTTCTGCGCAGGTTGCTCTCTGTTAAAGCTGTGGTGGAACTGTGCTGTGCTCC 901  
Db 1854 TTTTCTGCGCAGGTTGCTCTCTGTTAAAGCTGTGGTGGAACTGTGCTGTGCTCC 1913  
QY 902 ACHATTGCAATGATGTCATGTCCTCAAGCAAAAGTTTCTAAATAACCAAGAGGTC 961  
Db 1914 ATAAATGCAATGATGTCATGTCCTCAAGCAAAAGTTTCTAAATAACCAAGAGGTC 1973  
QY 962 TTCAATTTGAGACCAAGAGGCTGTGAGGAGGATTCACAAATCACTCCAGGCTGGCC 1021  
Db 1974 TTCAATTTGAGACCAAGAGGCTGTGAGGAGGATTCACAAATCACTCCAGGCTGGCC 2033  
QY 1022 TGGAGCCATAGGAGGATGATGCTGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1081  
Db 2034 TGGAGCCATAGGAGGATGATGCTGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2093  
QY 1082 ACCACAGCAGCTCTTCCCGCAGAGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1141

Db 2094 CTTCTGAGCAGCAC---ACGTGAGCAGTGGCATTTCTGTGTACCCCLYACAAGCAACCTT 2150  
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Db 2151 ---CATCCCAACAGAGTGGCCGAGGCT---CTCAGCTGCTGATGCTGGCTATGCT 2203  
QY 1202 TTACAGTGCATTTCTGAAGAGGAGACATCAAAAGAAATTAAGGATTTGTCACAGCTCTT 1261  
Db 2204 AAAGATCTTACTGCTCTCCCAACCAAAATTTCTCAGTTGTTGTTGTTTCAATAGCTTCCCTG 2263  
QY 1262 TTGAGAGAGGCTTAAAGGACAGGAGAGGAGGCTTCTCAATCTGTGGAAGAAATTAAGT 1321  
Db 2264 AGGATCTCAAGTGTCTTAAAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2323  
QY 1322 TTGTATTAATAAGATCACCAGCTAGTGTTCAGAGTTTACCAATGTACGTTATTTCCACTG 1381  
Db 2324 GCCTTCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2383  
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QY 1442 TGCAAGTGAGCACCTGATTCGCTTGGCTTGGCTTAACTCTAAAGCTCCATGTCTCTGGGCT 1501  
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QY 1502 AAAATCGTATAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTAACC 1561  
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QY 1562 AGAATCTTATGATGATACAACTGCTGTTTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1621  
Db 2561 GATGCTCTGTTTCTACAACTCAAGCTTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2620  
QY 1622 ACTTGTGCTGTGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1681  
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QY 1682 ATTTAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1741  
Db 2677 ATTTAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2733  
QY 1742 CTTATCTTCACTTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1801  
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QY 1802 CTCCTTTTGAATTAATACTGTTGGCTTTTCTAACTCTGTTAAATATATCTATTTTACC 1861  
Db 2793 CTCCTTTTGAATTAATACTGTTGGCTTTTCTAACTCTGTTAAATATATTTTATTTTACC 2852  
QY 1862 AAAGGATTTAAATATCTTTTATGACAACTTAGATCAACTATTTTATGCTTGGTAA--- 1919  
Db 2853 AAAGGATTTAAATATCTTTTATGACAACTTAGATCAACTATTTTATGCTTGGTAA--- 2912  
QY 1920 -ATTTTCTAAACACAACTTGTATAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1975  
Db 2913 TTTTCTTAAACAAATTTGTTATAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2972  
QY 1976 GTTGCCCTGAGCAAAAATACATATNTCCATCCCGAATGGTGTGCTAGAGTTGGATTA 2035  
Db 2973 GTTGCTCT-GACAAAAACATATGTAATTT-CTTCTGTATGGTGTGCTAGAGCTTAGCGTCA 3030  
QY 2036 CTTGCAATTTTAAAAA 2051  
Db 3031 TCTGCAATTTGAAAAGA 3046

RESULT 11

US-09-457-066-6

; Sequence 6, Application US/09457066

; Patent No. 6435673

; GENERAL INFORMATION:

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; APPLICANT: Gao, Zeren
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1035)
; OTHER INFORMATION: n = A,T,C or G
US-09-457-066-6

Query Match          34.8%; Score 734.4; DB 4; Length 1035;
Best Local Similarity 56.6%; Pred. No. 8.9e-178;
Matches 585; Conservative 261; Mismatches 188; Indels 0; Gaps 0;

Qy 37 ATGAGCCTCTTCGGGCTTCTCCTGGTGCATCTGCGCCGCGCCGAGACGAGGGACT 96
Db 1 ATGWSNYNTTYGGNYTNYTNYTACNWSNCGNYTNGCNGCARMGNCARGNACN 60

Qy 97 CAGCGGAATCCACCTGAGTAGTAATCCAGTTTCCAGCAACGAGAAACGAGACGA 156
Db 61 CARGCNGARWSNAAYTNNWSNNAARTTYCARTTYWSNWSNAAYAAARGARCARAYGN 120

Qy 157 GTACAAGATCCTCAGCATGAGAGAAATATTACTGTGTCTACTAATGGAAGATTTCACAGC 216
Db 121 GTNCARGAYCCNCAACGAYGARMGNATHACNGTNNWSNACNAAYGNNWSNATHCAYWSN 180

Qy 217 CCAGGTTTCTCATCTATCCAGAAATACCGTCTTGATGAGAGATTAGTAGCAGTA 276
Db 181 CCNMGNTTYCCNCAATCACTGAGTATCCAGAAATACCGTCTTGATGAGAGATTAGTAGCAGTA 240

Qy 277 GAGGAAATGTATGATGATCAACTTACCTTTGATGAAAGATTGGGCTTGAAGACCCAGAA 336
Db 241 GARGAAYGNTGATGATCACTTACCTTTGATGAAAGATTGGGCTTGAAGACCCAGAA 300

Qy 337 GATCAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 396
Db 301 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360

Qy 397 GGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 456
Db 361 GGNMGNTGGTGGGWSNNGNACNGTNCNGNAGNARCARATHWSNAAAGNAAACARATH 420

Qy 457 AGGATAGATTTGATCTGATGATATTTTCTCTGATGATGATGATGATGATGATGATGAT 516
Db 421 MGNATHMGNTTYGNTWSNGAYGATATYTYCCNWSNGAYGATGATGATGATGATGATGATGAT 480

Qy 517 AACATTGTGATGCCACATTCACAGAAAGCTGTGAGTCTCTCAGTGTGATGATGATGATGAT 576
Db 481 AAYATHGNTATGCCNARTTYACNGAGCNGTNNWSNCCNWSNNGTNTTNCNCCNWSNCCN 540

Qy 577 TTGCCACTGGACCTGCTTAATATGCTTAACTGCTTAACTGCTTAACTGCTTAACTGCTTAA 636
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Qy 637 CGATATCTTGAACACGAGAGATGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 696
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Qy 697 CAACCTTCTGGCAAGGCTTTTGTGTTTGAAGAAATCCAGAGTGGTGGATCTGAACCTT 756
Db 661 CARYTNTYNGGNAARGCNTTYGTNTTYGNGMGAARWSNMGNGTNGTNGAYTNAAYTNTN 720

Qy 757 CTAAACAGAGGAGTAAGATTATACAGCTGCACACCTCGTAACTCTCAGTGTCCATAAGG 816
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Qy 817 GAAGAACTAAAGAGAACCGATACCATTTTCTGCGCAGGTTGTCTCTCGTTAAACCGCTGT 876
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Qy 937 GTTACTAAATAATACCACGAGGTCCTTTCAGTTTGAGACCAAGACCGGTTCTCAGGGATTTG 996
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RESULT 12
US-09-706-968-6
; Sequence 6, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence derived from SBQ ID NOS: 1 and
; OTHER INFORMATION: 2
; NAME/KEY: misc_feature
; LOCATION: (1)...(1035)
; OTHER INFORMATION: n = A,T,C or G
US-09-706-968-6

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Query Match          34.8%; Score 734.4; DB 4; Length 1035;
Best Local Similarity 56.6%; Pred. No. 8.9e-178;
Matches 585; Conservative 261; Mismatches 188; Indels 0; Gaps 0;

Qy 37 ATGAGCCTCTTCGGGCTTCTCCTGGTGCATCTGCGCCGCGCCGAGACGAGGGACT 96
Db 1 ATGWSNYNTTYGGNYTNYTNYTACNWSNCGNYTNGCNGCARMGNCARGNACN 60

Qy 97 CAGCGGAATCCACCTGAGTAGTAATTCAGTTTCCAGCAACGAGAAACGAGACGA 156
Db 61 CARGCNGARWSNAAYTNNWSNNAARTTYCARTTYWSNWSNAAYAAARGARCARAYGN 120

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157 GTACAAGATCTCAGCATGAGAGATTAATTAATCTGTGTCTACTAATGAAAGTATTCACAGC 216
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Qy 217 CCAAGGTTTCTCATCTATCCAGAAATACCGTCTTGTATGGAGATAGTAGCAGTA 276
Db 181 CCNNGNTTYCCNCAAYCACTACCCNMGNAAYACNGTNTYNTGNGNNTYNTGNGNNTYNTG 240
Qy 277 GAGGAAATGTATGGATCAACACTTACGTTTGCATGAAAGATTTGGGTTGGAAGACCCAGAA 336
Db 241 GARGAAYGNTGTGATHCARYNACNTTYGAYGARMGNTTYGNTNGARGAYCCNGAR 300
Qy 337 GATGACATATGCAAGATGATTTGTAGAAATGTAGGAAACCCAGTGAATGAACATATTA 396
Db 301 GAYGAYATHTGYAARTAYGATTTGTNGARGTNGARGARCCNWSNGNACNAATHYTN 360
Qy 397 GGGCGCTGGTGTGCTTCTGCTACTGTACCAAGGAAACAGATTTCTAAAGGAAATCAAAIT 456
Db 361 GGNMGNTGGTGGGNGNAGNAGTNTCCNGNARCARATHSNAAAGGNAAYCARATH 420
Qy 457 AGGATAGATTTGTATCTGATGATATTTCTTCTGAAACGAGGTTCTGCATCCACTAC 516
Db 421 MGNATHMGNTTYGNTWSNGAYGARTATTTCCNWSNGARCCNGNTTYTGTATHTCAATY 480
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Qy 577 TTGCCATGACCTGCTTAAATATGCTATTAATCTGCTTGTAGTCTTGTGGAAGACCTTAT 636
Db 541 YTNCCNNTYNGAYTYNTNAAAYAGCNATHACNGCNTTYNSACNTYNTNGARGAYTYNATH 600
Qy 637 CGATATCTTGAACACAGAGATGCGAGTGTGACTTAGAAGATCTATATAGGCAACTTGG 696
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Qy 697 CAATCTCTGCAAGGCTTTGTTTGTGGAAGAAATCCAGAGTGTGAGTCTGAACCTT 756
Db 661 CARYTNTNGNAAAGCNTTYTGTNTTYGNNGNAARWSNMGNTGTNGAYTYNAAAYTN 720
Qy 757 CTAACAGAGAGGTAAGATTAACAGCTGCACACTCTGTAACCTCTCAGTGTCCATAAGG 816
Db 721 YTNACNGARGGNTMGNNTYNTATWSNTGYACNCCNMGNAAYTYTWSNGNTWSNATHMN 780
Qy 817 GAAGAACTAAAGAGAACGATACCATTTCTGCGCAGGTTGTCTCTGTTAAACCGCTGT 876
Db 781 GARGARYTNAARMGNACNGAYACNATHTTTGTGCGCGGNTGYTNTYNTGNTAARMGNTGY 840
Qy 877 GGTGGAACTGCTGCTGTCTCCCAATTTGCAATGCAATCTCAATGTCCTCCAGCAAA 936
Db 841 GNGGNAAYTYGCGNTGYTTCAYTAAYTYGAYGARTGYCARTGYTNCNWSNAAR 900
Qy 937 GTTACTAAATAATACCAGAGTCTCTCAGTTGAGACCAAGACCGGTGTGAGGGATG 996
Db 901 GTNACNAARAARTAYCAYGARGTYTNCARTYNMGNCCNARACNGGNTMNGNGNTN 960
Qy 997 CACAAATCACTACCGAGTGGCCTGAGGACCATGAGGAGTGTGACTGTGTGAGCAGA 1056
Db 961 CAYARWSNTYNTACNGAYTGNGNTNGARCAICAYGARGARTGYGATYGTGNTGYMN 1020
Qy 1057 GGGAGCACAGGAGG 1070
Db 1021 GGNWSNACNGGNGG 1034

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## RESULT 13

US-09-564-595D-6

; Sequence 6, Application US/09564595D

; Patent No. 6495668

; GENERAL INFORMATION:

; APPLICANT: Gilbert, Teresa

; APPLICANT: Hart, Charles E.

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; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence
; NAME/KEY: misc feature
; LOCATION: (1)-(1110)
; OTHER INFORMATION: n = A,T,C or G
US-09-564-595D-6

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Query Match 8.4%; Score 177.6; DB 4; Length 1110;

Best Local Similarity 34.5%; Pred. No. 8.2e-36;

Matches 349; Conservative 194; Mismatches 395; Indels 75; Gaps 6;

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Qy 118 AGTAATTCAGTTTCCAGCAACAGGAACAGACGAGTACAGATCCTCAGCATGAG 177
Db 100 MGNAAAYGCNAAYTYNMGMNGAYGARWSNAAAYCAITYTNACNGAYTYNTYMGNGMNGAY 159
Qy 178 AGAATTAATTAATCTGCTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTCATACTAT 237
Db 160 GARACNATHCARGTNAARGGNAAYGNGTAYGTCNARWSNCCNMGNTTYCCNAAWSTAY 219
Qy 238 CCAAGAAATACGCTCTGATGAGATTAAGTACAGTACAGTACAGGAAATGATGATGATACAA 297
Db 220 CCNMGNAAYTYNTYTNACNTGGMNTYNTCAYS---NCARGAARAYACNMGNATHCAR 276
Qy 298 CTTAGCTTGTGATGAAAGATTTGGGCTTGAAGACCAAGATGACATATGCAAGTATGAT 357
Db 277 YTNGTNTTYGAYAAVCARTTYGNTNGARGCNGARBAAYATHTGYMGNATYAY 336
Qy 358 TTTGTAGAGTTGAGAAACCCAGTGTGGAAC-----TATATTAGGCGCTGTGTGCT 411
Db 337 TTYTNGARGTNGARGAYATHWSNGARACNWSNACNATHATHMNGNMGNTGTGTGCGN 396
Qy 412 TCTGCTACTGTACCAAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTTGTA 471
Db 397 CAYARGARGTNCNCCNMGNAATHARWSNMGNAACNAYCARATHARATHACNTTYAAR 456
Qy 472 TCTGATGAATATTTCTCTTGAACCCAGGGTTCTGCACTCCATCACTACAACTTGC----- 525
Db 457 WSNAGAYATYATYTGTCNAAACCCNGNTTYAARATHTATYATYWSNYNTYNGARGAY 516
Qy 526 -----ATGCCAATTCACAGAGCTGTGAGTCTTCACTGCTAC----- 565
Db 517 TTYCARCCNGCNGCNGCNGSNAGARACNAAAYTGGGARSNGNTNACNWSNATHWSNGN 576
Qy 566 -----CCCTTTCAGCTTTGCCACTTGGACCTCTCTTAATAAT 600
Db 577 GTNWSNTAYAAWWSNCCNWSNGTNAACNGAYCCNACNTYTNATHGNCNGAYGVCNTYNGAYAR 636
Qy 601 GCTATAACTGCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACCAAGAGATGG 660
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Qy 661 CAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTGT 720
Db 697 CARGARGAYTYTNGARPAATATGTATYTNCAAYACNCCNMGNTYMGNGMNGWSNTAYCAY 756
Qy 721 TTTGGAAGAAATCCAGAGTGTGATCTGAACCTTCTTAACAGAGGAGGTAAGATTATAC 780

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Wed Nov 26 13:03:28 2003

Db 757 GAYMGNAR-----WSNAARGTNGAYYNGAYMGNMYNAAAYGAYGAYCNWAARMGNTAY 810  
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 Qy 841 ATTCTTGGCCAGGTCTCTCTGTTAAAGCTGTGGTGGGAACTGTGCTGTGTGCTC 900  
 Db 871 GNTTCTTTCYCNMGTGTGTYNTGNTNCARWNTGTGGNGNATGTGGNTGTGNGACN 930  
 Qy 901 CACAATTCGAATGTCAATGTGTCCCAAGCAAAATTTACTAAAAATACACAGGTC 960  
 Db 931 GTNAAATCGMGNWSNTGYACNTGYAAYWSNGNAARACNGTNAARAAETAYCAYARGTN 990  
 Qy 961 CTTCAGTTGAGACC-----AAAGACCGGTGTGTCAGGGGATTCACAAATCACTCACC 1011  
 Db 991 YTNCAATTVGARCNGGNCAYATHAARMGNMGNMNGNCNAARACNATGGCNYTNGTN 1050  
 Qy 1012 GACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGGACAC 1064  
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RESULT 14

US-09-540-224-3  
 ; Sequence 3, Application US/09540224  
 ; Patent No. 6468543  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gilbertson, Debra G.  
 ; APPLICANT: Hart, Charles E.  
 ; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
 ; FILE REFERENCE: 00-28  
 ; CURRENT APPLICATION NUMBER: US/09/540,224  
 ; PRIOR FILING DATE: 2000-03-31  
 ; EARLIER FILING DATE: 2000-02-04  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1472  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1205)  
 US-09-540-224-3

Query Match 5.6%; Score 117.8; DB 4; Length 1472;  
 Best Local Similarity 50.9%; Pred. No. 1.6e-20; Mismatches 402; Indels 75; Gaps 6;  
 Matches 494; Conservative 0;  
 Qy 169 CAGCATGAGAGAAATTTACTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTCTCT 228  
 Db 243 CAGAGAGAGAGAAATTTACTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTCTCT 302  
 Qy 229 CATACTTATCCAGAAATACCGTCTTGATGAGATTAAGTACAGTACAGGAAATGTA 288  
 Db 303 ACACGTACCCAGGAACCTGTTCTGACATGTTGGCTCCGTTCC---CCAGAGAAACA 359  
 Qy 289 TGGATACACTTACCTTTGATGAAGATTTGGGCTTGAAGCCAGAGATGACATATGC 348  
 Db 360 CGATACAACTCTCTTTGACCATCAATTCGGACTAGAGAGAGAGAAATGACATTTGT 419  
 Qy 349 AGATATGATTTTGTAGAAGTGTAGAGAACCCAGTGTATGGA-----CTATATAGGGCGC 402  
 Db 420 AGGTATGACTTTGTGGAAGTGTGAAGAGTCTTCAGAGAGAGAGAGAGAGAGAGAG 479  
 Qy 403 TGTGTGGTCTTGGTACTGTATCCAGGAAACACAGATTTCTAAAGGAATCAATATAGGATA 462  
 Db 480 TGTGTGGCCACAGAGAGATCCCTCCAGGATTAAGTCAAGACACACAGATTAATATC 539

Qy 463 AGATTGTATCTGATGAATATTTTCTTGTGAACCGAGGTTCTGCTATCCACTACACATT 522  
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 Qy 523 GT----CATGCCCAATTCACAGAGAGTGTGAGTCTTCACTAGTCTACCCCTTCAGTTT 578  
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 Qy 579 GCCACTGGACCTGCTTA-----GCTCAATTAACGAGCCCACTCTCACTGCTGATGCC 595  
 Db 650 TTCTCTGGGGTCTCTATCACTCTCAATTAACGAGCCCACTCTCACTGCTGATGCC 719  
 Qy 596 ----ATAATGCTATTAACCTCTTAGTACCTTGAAGACCTTATTGATATCTTGAACA 651  
 Db 720 CTGGACAAACAGTGTGAGAAATTCGATACCGTGAAGATCTACTTAAGCACTTCAATCCA 779  
 Qy 652 GAGAGATGCGAGTGTGAGCTTTAGAGATCTATATAGGCCAACTTTGGCAACTCTTGGCAAG 711  
 Db 780 GTGTCTTGGCAAGATGATCTGGAGAAATTTGTATCTGGACACCCCTCATTTATAGAGCAGG 839  
 Qy 712 GCTTTTGTCTTGGGAAGAAATTCAGAGTGTGATCTGAACCTTCTTAACAGAGAGAGTA 771  
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 Qy 832 ACCGATACCAATTTCTGGCCAGGTTGTCTCTCTGTTTAAACGCTGTGTGGGAACTGTGCC 891  
 Db 954 ACCAATGCACTCTTCTTCCACAGATSCCTCTCTGTGAGCGGCTGTGTGGTCAACTGTGT 1013  
 Qy 892 TGTGTCTCCACAATTCGAATGTAATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAAATAC 951  
 Db 1014 TGGGAACTGTCACTGTGAAGTCTCTGACATGCGAGCTCAGGAGAGACAGTGAAGAGTAT 1073  
 Qy 952 CAGAGGTCTCTCAGTTGAGACC-----AAAGACCGGTGTGAGGAGTGTGCAAAA 1002  
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 Qy 1003 TCACTCAGCAGCTGGCCCTGGAGACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGC 1062  
 Db 1134 GCTCTTGTGATATCCAGCTGGATCATCATGAGCGATGTGACTGTATCTGCACTCAAGA 1193  
 Qy 1063 ACAGGAGGATA 1073  
 Db 1194 CCACCTCGATA 1204

RESULT 15  
 US-09-564-595D-52  
 ; Sequence 52, Application US/09564595D  
 ; Patent No. 6495668  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gilbert, Teresa  
 ; APPLICANT: Hart, Charles E.  
 ; APPLICANT: Sheppard, Paul O.  
 ; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF4  
 ; FILE REFERENCE: 99-19  
 ; CURRENT APPLICATION NUMBER: US/09/564,595D  
 ; PRIOR FILING DATE: 2000-05-03  
 ; PRIOR APPLICATION NUMBER: US 09/304,216  
 ; PRIOR FILING DATE: 1999-05-03  
 ; PRIOR APPLICATION NUMBER: US 60/164,463  
 ; PRIOR FILING DATE: 1999-11-10  
 ; PRIOR APPLICATION NUMBER: US 60/180,169  
 ; PRIOR FILING DATE: 2000-02-04  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 52  
 ; LENGTH: 1472  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus

FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (93)...(1205)  
US-09-564-595D-52

Query Match 5.6%; Score 117.8; DB 4; Length 1472;  
Best Local Similarity 50.9%; Pred. No. 1.6e-20;  
Matches 494; Conservative 0; Mismatches 402; Indels 75; Gaps 6;

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Db 1194 CCACCTCGATA 1204

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Qy 892 TGTGTCTCCACAAATTCGAATGATGTCATGTCCTCCCAAGCAAGTTACTTAAATAATAC 951  
Db 1014 TGGGAATGTCAACTGGAAGTCTGCAATGTCAGCTCAGGGAGACAGTGAAGAGTAT 1073  
Qy 952 CACGAGTCTTCTAGTTGAGACC-----AAAGCCGGTGTACAGGGGATTGCACAA 1002  
Db 1074 CATGAGTATTGAAGTTTGGACCTGGACATTTCAAGAGAAGGGCAAGCTAAGATATG 1133  
Qy 1003 TCATCACCAGCTGGCCCTGGAGCACATGAGAGTGTGACTGTGTGTCAGAGGAGC 1062  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
13382.717 Million cell updates/sec

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Perfect score: 2108  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues 4380138

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2103.6	99.8	2108	10	US-09-852-209A-2
2	2103.6	99.8	2108	14	US-10-131-600-2
3	1979.4	93.9	2825	14	US-10-178-442-1
4	1979.4	93.9	2839	11	US-09-796-753-5
5	1979.4	93.9	2849	10	US-09-978-295A-487
6	1979.4	93.9	2849	10	US-09-978-697-487
7	1979.4	93.9	2849	10	US-09-978-192A-487
8	1979.4	93.9	2849	10	US-09-999-832A-487
9	1979.4	93.9	2849	11	US-09-978-189-487
10	1979.4	93.9	2849	11	US-09-978-608A-487
11	1979.4	93.9	2849	11	US-09-978-585A-487
12	1979.4	93.9	2849	11	US-09-978-191A-487
13	1979.4	93.9	2849	11	US-09-978-403A-487
14	1979.4	93.9	2849	11	US-09-978-564A-487
15	1979.4	93.9	2849	11	US-09-999-833A-487
16	1979.4	93.9	2849	11	US-09-981-915A-487

17	1979.4	93.9	2849	11	US-09-978-824-487	Sequence 487, App
18	1979.4	93.9	2849	11	US-09-918-585A-487	Sequence 487, App
19	1979.4	93.9	2849	11	US-09-978-423A-487	Sequence 487, App
20	1979.4	93.9	2849	11	US-09-978-193A-487	Sequence 487, App
21	1979.4	93.9	2849	11	US-09-999-830A-487	Sequence 487, App
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24	1979.4	93.9	2849	11	US-09-978-643A-487	Sequence 487, App
25	1979.4	93.9	2849	12	US-09-978-375A-487	Sequence 487, App
26	1979.4	93.9	2849	12	US-09-978-188A-487	Sequence 487, App
27	1979.4	93.9	2849	12	US-09-978-298A-487	Sequence 487, App
28	1979.4	93.9	2849	12	US-10-137-870-285	Sequence 285, App
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37	1979.4	93.9	2849	12	US-10-141-698-285	Sequence 285, App
38	1979.4	93.9	2849	12	US-10-141-702-285	Sequence 285, App
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41	1979.4	93.9	2849	12	US-10-142-432-285	Sequence 285, App
42	1979.4	93.9	2849	12	US-10-142-767-285	Sequence 285, App
43	1979.4	93.9	2849	12	US-10-143-031A-487	Sequence 487, App
44	1979.4	93.9	2849	12	US-10-143-033-285	Sequence 285, App
45	1979.4	93.9	2849	12	US-10-144-994-285	Sequence 285, App

ALIGNMENTS

RESULT 1

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; Sequence 2, Application US/09852209A  
; Patent No. US20020164687A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETSHOLZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,  
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/852,209A  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2108  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (2002)  
; OTHER INFORMATION: can be a, c, g or t

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; NAME/KEY: unsure
; LOCATION: (2065)
; OTHER INFORMATION: can be a, c, g or t
; NAME/KEY: unsure
; LOCATION: (2070)
; OTHER INFORMATION: can be a, c, g or t
; NAME/KEY: unsure
; LOCATION: (2089)
; OTHER INFORMATION: can be a, c, g or t
US-09-852-209a-2

Query Match      99.8%; Score 2103.6; DB 10; Length 2108;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCGCGTGAGTCAGCTCTCACCCCGAGTCAGCCCAATGAGCCTCTTCGGGCTCTCCTG 60
Db 1 CCCCGCGTGAGTCAGCTCTCACCCCGAGTCAGCCCAATGAGCCTCTTCGGGCTCTCCTG 60

QY 61 GTGACATCTGCCCTGGCGGCGGACAGACAGGGGACTCAGGCGGAATCCAACTCAGTAGT 120
Db 61 GTGACATCTGCCCTGGCGGCGGACAGACAGGGGACTCAGGCGGAATCCAACTCAGTAGT 120

QY 121 AAATTCAGTTTTCAGCAACAAGAAACAGAACGAGTACAGATCCTCAGCATGAGAGA 180
Db 121 AAATTCAGTTTTCAGCAACAAGAAACAGAACGAGTACAGATCCTCAGCATGAGAGA 180

QY 181 ATTATTACTGTCTACTTAATGGAAGTATTACAGCCCAAGTTTCTCATCTTATCCA 240
Db 181 ATTATTACTGTCTACTTAATGGAAGTATTACAGCCCAAGTTTCTCATCTTATCCA 240

QY 241 AGAAATACGGTCTTTGGTATGAGATTAGTAGCAGTAGAGGAAATGTATGGATCAACTT 300
Db 241 AGAAATACGGTCTTTGGTATGAGATTAGTAGCAGTAGAGGAAATGTATGGATCAACTT 300

QY 301 ACCTTTGATGAAGATTGGCTTTGAAGACCCAGACATGACATATGCAAGTATGATTTT 360
Db 301 ACCTTTGATGAAGATTGGCTTTGAAGACCCAGACATGACATATGCAAGTATGATTTT 360

QY 361 GTAGAAGTGTAGGAACCCAGTGATGGAATATATTAGGGCGCTGGTGGTCTTGGTACT 420
Db 361 GTAGAAGTGTAGGAACCCAGTGATGGAATATATTAGGGCGCTGGTGGTCTTGGTACT 420

QY 421 GTACCAAGAAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATGAA 480
Db 421 GTACCAAGAAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATGAA 480

QY 481 TATTTTCTCTGAAACCAAGGTTCTGCATCCACTACACATTTGTATGCAACAAATTCACA 540
Db 481 TATTTTCTCTGAAACCAAGGTTCTGCATCCACTACACATTTGTATGCAACAAATTCACA 540

QY 541 GAAAGCTGTGAGTCCCTTCAGTGCTACCCCTTCAGCTTTGGCACCTGGACCTGCTTAATAAT 600
Db 541 GAAAGCTGTGAGTCCCTTCAGTGCTACCCCTTCAGCTTTGGCACCTGGACCTGCTTAATAAT 600

QY 601 GCTATAACGCTTTAGTACCTTGGGAAGACCTTATTCGATCTTTGAAACAGAGAGATGG 660
Db 601 GCTATAACGCTTTAGTACCTTGGGAAGACCTTATTCGATCTTTGAAACAGAGAGATGG 660

QY 661 CAGTTGACCTTAGAAGATCTATATAGGCCAACTTGGCACTTCTTGGCAAGGCTTTTGT 720
Db 661 CAGTTGACCTTAGAAGATCTATATAGGCCAACTTGGCACTTCTTGGCAAGGCTTTTGT 720

QY 721 TTTTGGAGAAAAATCCAGAGTGGTGAATCTGAACCTTCTAACAGAGGAGGTAAAGTTATAC 780
Db 721 TTTTGGAGAAAAATCCAGAGTGGTGAATCTGAACCTTCTAACAGAGGAGGTAAAGTTATAC 780

QY 781 AGCTGCAACCTCGTAACTTCTCAGTGTCCATTAAGGAAGAACTAAAGAGAACCGATACC 840
Db 781 AGCTGCAACCTCGTAACTTCTCAGTGTCCATTAAGGAAGAACTAAAGAGAACCGATACC 840

QY 841 ATTTTCTGGCGAGTCTCTCTCTGTTAAACGCTGTGGGACTGTGCTCTGTGCTC 900
Db 841 ATTTTCTGGCGAGTCTCTCTCTGTTAAACGCTGTGGGACTGTGCTCTGTGCTC 900
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Db 901 CACAAATTGCAATGAATGTCAATGTGTCCAGCAAAAGTTACTTAAAAATACACAGAGTC 960
QY 961 CTTTCAGTTGAGACCAAAAGACCGGTGTGAGGGGATTTGCACAATCACTCACCGAGTGGCC 1020
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Db 1141 TATGCGTTATCTCCATCTTAATCTCAGTTGTGTTTGTCTTCAAGGACCTTTCATCTTCAGGA 1200

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Db 1261 TTTTGAGAGGAGGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGGAAAGAAATTAAT 1320

QY 1321 GTTGTATTAATAATAGATCACCAGCTAGTTTTCAGAGTTTACCATGTACGTATTCACATAGCTG 1380
Db 1321 GTTGTATTAATAATAGATCACCAGCTAGTTTTCAGAGTTTACCATGTACGTATTCACATAGCTG 1380

QY 1381 GGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTGCTAGTACAGAGAAATAACT 1440
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QY 1441 GTGCAAGTGAGACCTGATTCGGTTCGCTTAACTCTAAAGCTCCATGCTCTGGGCC 1500
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Db 1561 CAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTA 1620

QY 1621 AACTTGTGTCRTGCTGATAGGACAGACTGGATTTTTTTCATATTTTCTTATTAATAATTTCTGC 1680
Db 1621 AACTTGTGTCRTGCTGATAGGACAGACTGGATTTTTTTCATATTTTCTTATTAATAATTTCTGC 1680

QY 1681 CATTTAGAAAGAGAGAACTACATTTCTATGTTTGGAGAGATTAACCTGAAAGAGAGTG 1740
Db 1681 CATTTAGAAAGAGAGAACTACATTTCTATGTTTGGAGAGATTAACCTGAAAGAGAGTG 1740

QY 1741 GCCTTATCTTCACTTTATTCGATTAAGTCAGTTTATTTGTTTTCATTTGTTGTCATATTTTATAT 1800
Db 1741 GCCTTATCTTCACTTTATTCGATTAAGTCAGTTTATTTGTTTTCATTTGTTGTCATATTTTATAT 1800

QY 1801 TCTCTCTTTTGCATTTAACTGTTGGCTTTTCTAACTCTGCTTAAATATATATCTATTTTTTAC 1860
Db 1801 TCTCTCTTTTGCATTTAACTGTTGGCTTTTCTAACTCTGCTTAAATATATATCTATTTTTTAC 1860

QY 1861 CAAAGGTATTTAATTTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGTGTA 1920
Db 1861 CAAAGGTATTTAATTTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGTGTA 1920

QY 1921 TTTTCTTAAACAAATTTGTTATGACAGAGGAAACAAAGATGGATATATAAATAATTTGTTC 1980
Db 1921 TTTTCTTAAACAAATTTGTTATGACAGAGGAAACAAAGATGGATATATAAATAATTTGTTC 1980
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Db |||||
2041 ATTTTAAAAAACCTGAAATGGGAANGGAANTTGGTAAGTTGGCCCAANCTTTTGTGAAA 2100
QY 2101 ATAATTAA 2108
Db |||||
2101 ATAATTAA 2108
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## RESULT 2

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US-10-131-600-2
; Sequence 2, Application US/10131600
; Publication No. US20030082670A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/10/131,600
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/1108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2108
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2002)
; OTHER INFORMATION: can be a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2065)
; OTHER INFORMATION: can be a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2070)
; OTHER INFORMATION: can be a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2089)
; OTHER INFORMATION: can be a, c, g or t
US-10-131-600-2
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Query Match 99.8%; Score 2103.6; DB 14; Length 2108;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCCCGCCGTGAGTGAGCTCTCACCCAGTCAGCAAAATGAGCCCTCTTCGGGCTTCTCCTG 60
Db |||||
1 CCCCGCCGTGAGTGAGCTCTCACCCAGTCAGCAAAATGAGCCCTCTTCGGGCTTCTCCTG 60
QY 61 GTGACATCTGCCCTGGCCGGCCAGAGACGAGGACTCAGCGGGAATCCCAACCTGAGTAGT 120
Db |||||
61 GTGACATCTGCCCTGGCCGGCCAGAGACGAGGACTCAGCGGGAATCCCAACCTGAGTAGT 120
QY 121 AAAATTCACAGTTTCCAGCAAAACAAGAAACAGAACGAGAGTACAAGATCCTCAGCATGAGAGA 180
Db |||||
121 AAAATTCACAGTTTCCAGCAAAACAAGAAACAGAACGAGAGTACAAGATCCTCAGCATGAGAGA 180
QY 181 ATTATTACTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCCTCATCTATATCCA 240
Db |||||
181 ATTATTACTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCCTCATCTATATCCA 240
QY 241 AGAAATACGGTCTTGGTATGGAGATAGTAGCAGTAGAGGAAAAATGATGGATACAACTT 300
Db |||||
241 AGAAATACGGTCTTGGTATGGAGATAGTAGCAGTAGAGGAAAAATGATGGATACAACTT 300
QY 301 ACGTTTGTGAAAGATTTTGGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATGATTTT 360
Db |||||
301 ACGTTTGTGAAAGATTTTGGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATGATTTT 360
QY 361 GTAGAAAGTTGAGAAACCCAGTGTATGAACTATATATTAGGCGCTGGTGTCTGTGACT 420
Db |||||
361 GTAGAAAGTTGAGAAACCCAGTGTATGAACTATATATTAGGCGCTGGTGTCTGTGACT 420
QY 421 GTACAGGAAACACAGATTTCTAAAGGAATCAAAATAGGATAAGATTCTGATCTGATGAA 480
Db |||||
421 GTACAGGAAACACAGATTTCTAAAGGAATCAAAATAGGATAAGATTCTGATCTGATGAA 480
QY 481 TATTTTCTCTTGAACCCAGGTTCTGCATCCACTCAACATGTGTATGTCACCAATTCACA 540
Db |||||
481 TATTTTCTCTTGAACCCAGGTTCTGCATCCACTCAACATGTGTATGTCACCAATTCACA 540
QY 541 GAAGCTGTGAGTCCTTCAGTGTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAAT 600
Db |||||
541 GAAGCTGTGAGTCCTTCAGTGTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAAT 600
QY 601 GCTATAACTGCCCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACACAGAGATGG 660
Db |||||
601 GCTATAACTGCCCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACACAGAGATGG 660
QY 661 CAGTTGGACTTAGAAGATCTATATAGGCCAACTTGCAACTCTTTCGGCAAGGCTTTGTT 720
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721 TTTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAAGATTATAC 780
QY 781 AGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAACCGATACC 840
Db |||||
781 AGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAACCGATACC 840
QY 841 ATTTTCTGGCCAGGTTGTCTCTGTTTAAACCGCTGTGGGAACTGTCCCTGTGTCTC 900
Db |||||
841 ATTTTCTGGCCAGGTTGTCTCTGTTTAAACCGCTGTGGGAACTGTCCCTGTGTCTC 900
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Db |||||
901 CACAATTCGAATGAATGTCAATGTCTCCCAAGCAAAAGTTTACTTAAAAAATACCACGAGTTC 960
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961 CTTCAGTTTGAGCAAAAGACCGGTGTCTAGGGGATTCACAATCACTCACTCCACGCTGGCC 1020
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1021 CTGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGAGCACAGGAGGATAGCCGAT 1080
QY 1081 CACCACGACGAGCTCTTGGCCACAGAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAACG 1140
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1141 TATCGGTATCTCCATCTTATCTCAGTGTGTTGCTTCAAGACCTTTCATCTTCAGA 1200  
1201 TTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTAGGAGTTGTGCAACGCTCT 1260  
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1261 TTTGAGAGAGGCTTAAGGACAGAGAAAGGCTTCAATCGTGGAAAGAAATTAAT 1320  
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1321 GTTGATTAAATAGATCACCGCTAGTTTCAGAGTTTACCATGTACGTATTTCCACTAGCTG 1380  
1381 GGTTCGTATTTTCAGTCTTTTCGATACGGCTTAGGTAATGTACGTACAGGAAAGAACT 1440  
1381 GGTTCGTATTTTCAGTCTTTTCGATACGGCTTAGGTAATGTACGTACAGGAAAGAACT 1440  
1441 GTGCAAGTGCACCTGATTCGGTTCCTGCTTAACCTTAAGCTCCATGTCTGGGCC 1500  
1441 GTGCAAGTGCACCTGATTCGGTTCCTGCTTAACCTTAAGCTCCATGTCTGGGCC 1500  
1501 TAAATCGTATAAATCTCGATTTTCTGCTCATATTTTCATATGTCAATGTAAAC 1560  
1501 TAAATCGTATAAATCTCGATTTTCTGCTCATATTTTCATATGTCAATGTAAAC 1560  
1561 CAGAACATTCATGTACTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATGAATTA 1620  
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1621 AACTGTGTCRTGCTGATAGGACAGACTGATTTTTCATATTTTCATATTTAAATTTCTGC 1680  
1681 CATTTAGAGAGAGAACTACATTTTCATGTTTGGAGAGATAAACCCTGAAAGAGAGTG 1740  
1681 CATTTAGAGAGAGAACTACATTTTCATGTTTGGAGAGATAAACCCTGAAAGAGAGTG 1740  
1741 GCCTATCTCTCTTTATCGATAAGTCACTTTATTTGTTTCATTTGTTGATCAATTTTATAT 1800  
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1801 TCTCCCTTTGACATTATACTGTTGGCTTTTCTAATCTTGTAAATATATCTATTTTAC 1860  
1861 CAAAGGTATTTAATATCTTTTATGCAACTTAGATCAACTATTTTATGCTTGGTAAA 1920  
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1981 CTTGGACAAAATACATGATATNTCCATCCCGGAATGGTCTAGAGTTGATTAACCTGC 2040  
1981 CTTGGACAAAATACATGATATNTCCATCCCGGAATGGTCTAGAGTTGATTAACCTGC 2040  
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2041 ATTTTAAACAACTGAATTTGGGAAGGAANTTGGTAAAGTTTGGCCAAANCTTTTTGAAA 2100  
2101 ATAATTA 2108  
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US-10-178-442-1  
; Sequence 1, Application US/10178442  
; Publication No. US20030113870A1  
; GENERAL INFORMATION:  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Kuo, Sophia S.  
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1  
; FILE REFERENCE: 11669.112USD2  
; CURRENT APPLICATION NUMBER: US/10178,442  
; CURRENT FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: US 09/265,686  
; PRIOR FILING DATE: 1999-03-10  
; PRIOR APPLICATION NUMBER: US 09/184,216  
; PRIOR FILING DATE: 1998-11-02  
; PRIOR APPLICATION NUMBER: US 09/040,220  
; PRIOR FILING DATE: 1998-03-17  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2825  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2689)..(2689)  
; OTHER INFORMATION: Any nucleotide  
US-10-178-442-1

Query Match 93.9%; Score 1979.4; DB 14; Length 2825;  
Best Local Similarity 97.7%; Pred. No. 0;  
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCGCGCGTGAGTGAGCTCTCACCCAGTCAGCCAAATAGCCTCTTCGGGCTTCTCCTGG 61  
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QY 122 AATTCGAGTTTTCCAGCACAGGACAGAACGGAGTACAAGATCCTCAGCATGAGAGAA 181  
DB 344 AATTCGAGTTTTCCAGCACAGGACAGAACGGAGTACAAGATCCTCAGCATGAGAGAA 403  
QY 182 TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTCATCTTATCCAA 241  
DB 404 TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTCATCTTATCCAA 463  
QY 242 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAACTTA 301  
DB 464 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAACTTA 523  
QY 302 CGTTTGTATCAAGATTTGGGCTTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 361  
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QY 362 TAGAAGTTGAGGAACCCAGTGTATGGAACCTATATTAGGGCGCTGGTGTGTTCTGTTACTG 421  
DB 584 TAGAAGTTGAGGAACCCAGTGTATGGAACCTATATTAGGGCGCTGGTGTGTTCTGTTACTG 643  
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DB 704 ATTTTCTCTTCAACAGGGTTCTGCATCCCACTACAACTTTCATGTCATGCCAATTCACAG 763  
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DB 764 AAGCTGTGAGTCTCTTCAAGTGTACCCCTTTCAGCTTTGCACTGGACCTGCTTAAATG 823  
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Db 1544 TTGTATTAATAGATCACCAGCTAGTTTTCAGAGTTTACCATGTACGTATTCCTAGCTGG 1603  
QY 1382 GTTCTGTATTTTCAGTTCTTCGATACGGCTTAGGGTAAATGTGTCAGTACAGGAAAAAATG 1441  
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QY 1502 AAAATCGTATAAACTCGATTTTCTGATTTTCTGCTCATATTCATATGTAAACC 1561  
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QY 1562 AGAATCTATGTACTACAACTGGTTTAAAAAGGAACATGTTGCTATGAATTA 1621  
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Db 1844 ACTTGTGCTGCTGATAGGACAGCTGATTTTCAATTTCTTATTAATAATTTCTGCC 1903  
QY 1682 ATTTAGAAGAGAGAACTTACATTTCTGTTGGAAGAGATAAACCCTGAAAGAGATGG 1741

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Db 1964 CCTTATCTTCCATTTATCGATAAGTCAGTTTATTTTGTTCATTTGTGTACATTTTATATT 2023  
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RESULT 4  
US-09-796-753-5  
; Sequence 5, Application US/09796753  
; Publication No. US20030027998A1  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A.  
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
; FILE REFERENCE: 7853-227-999  
; CURRENT APPLICATION NUMBER: US/09/796, 753  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 09/183, 175  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: 09/223, 094  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/223, 546  
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; PRIOR APPLICATION NUMBER: 09/409, 634  
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; PRIOR APPLICATION NUMBER: 09/474, 072  
; PRIOR FILING DATE: 1999-12-29

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, PRIOR APPLICATION NUMBER: 09/514,010
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, PRIOR APPLICATION NUMBER: 09/516,745
, PRIOR FILING DATE: 2000-03-01
, PRIOR APPLICATION NUMBER: 09/572,002
, PRIOR FILING DATE: 2000-05-14
, PRIOR APPLICATION NUMBER: 09/587,993
, PRIOR FILING DATE: 2000-06-19
, PRIOR APPLICATION NUMBER: 09/599,596
, PRIOR FILING DATE: 2000-06-22
, PRIOR APPLICATION NUMBER: 09/630,334
, PRIOR FILING DATE: 2000-07-31
, PRIOR APPLICATION NUMBER: 09/606,565
, PRIOR FILING DATE: 2000-06-29
, PRIOR APPLICATION NUMBER: 09/606,317
, PRIOR FILING DATE: 2000-06-29
, PRIOR APPLICATION NUMBER: 09/665,666
, PRIOR FILING DATE: 2000-09-20
, PRIOR APPLICATION NUMBER: 09/677,751
, PRIOR FILING DATE: 2000-09-30
, NUMBER OF SEQ ID NOS: 162
, SEQ ID NO 5
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, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, NAME/KEY: CDS
, LOCATION: (288) ... (1322)
US-09-796-753-5

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Qy	122	AATTCCAGTTTTCCAGCAACACAGGAACAGACGAGGTACAGATGCTTCAGCATGAGAA 181		
Db	373	AATTCCAGTTTTCCAGCAACACAGGAACAGACGAGGTACAGATGCTTCAGCATGAGAA 432		
Qy	182	TTATTACTGTGCTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA 241		
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Qy	242	GAATACGGTCTTGATATGGAGATTAGTACAGTAGAGGAAATGATGGATACAACCTTA 301		
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Qy	302	CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAGAATGACATATGCAAGTATGATTTTG 361		
Db	553	CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAGAATGACATATGCAAGTATGATTTTG 612		
Qy	362	TAGAAGTTGAGGAACCCAGTGATGGAACATAATTAGGCGCTGGTGGGTTCTGGTACTG 421		
Db	613	TAGAAGTTGAGGAACCCAGTGATGGAACATAATTAGGCGCTGGTGGGTTCTGGTACTG 672		
Qy	422	TACCAGGAAACAGATTTCTAAAGGAATCAAAATAGGATGAAGATTTGTTATCTCATGAAT 481		
Db	673	TACCAGGAAACAGATTTCTAAAGGAATCAAAATAGGATGAAGATTTGTTATCTCATGAAT 732		
Qy	482	ATTTTCCTTCTGAACCGAGGTTCTGCATCCACTACACATTTGTCATGCGCAAAATTCACAG 541		
*Db	733	ATTTTCCTTCTGAACCGAGGTTCTGCATCCACTACACATTTGTCATGCGCAAAATTCACAG 792		
Qy	542	AAGCTGTGAGTCCCTTCACTGCTACCCCTTCAGCTTTGCGACCTGGACCTGCTTAATTAATG 601		
Db	793	AAGCTGTGAGTCCCTTCACTGCTACCCCTTCAGCTTTGCGACCTGGACCTGCTTAATTAATG 852		

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QY	662	AGTTGG	ACTTTAGAGATCTATATAGGCCAACTTTGGCAACTTCTTGGCAAGGCTTTTGTGTTT	721
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QY	722	TTGGA	AGAAAATCCAGAGTGGTGGATCTGAACCTTTCTTAAACAGAGGAGGTAAAGATTATACA	781
DB	973	TTGGA	AGAAAATCCAGAGTGGTGGATCTGAACCTTTCTTAAACAGAGGAGGTAAAGATTATACA	1032
QY	782	GCTG	CACACCTCTGTAACCTTCTCAGTGTCTCATATAGGAGAACTTAAAGAGAACCGATACCA	841
DB	1033	GCTG	CACACCTCTGTAACCTTCTCAGTGTCTCATATAGGAGAACTTAAAGAGAACCGATACCA	1092
QY	842	TTTTCT	TGGCCAGGTGTCTCCTCGTTTAAACCGCTGTGGTGGGAACCTGTGCTGTGTCTCC	901
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QY	1622	ACTT	GTGTCGTGCTGATAGAGACAGCTGGATTTTTTTCATATTTCTTATTTAAAAATTTCTGCC	1681
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Db 2288 TTTTAAACACCTGAAAT--GGAATAGATTGTTAGTT--GCAAGACTTTTGTGAAA 2341  
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## RESULT 5

US-09-978-295A-487  
; Sequence 487, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
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; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
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66	PRIOR FILING DATE: 1998-05-13
67	PRIOR APPLICATION NUMBER: 60/085323

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Db 1870 ACTGTGTCRGTCTGATAGGACAGATGGAATTTTTCATATTTCTTATTTAAATTTCTGCC 1929  
QY 1682 ATTTAGAAGAGAACTACATTCATGTTGTTGAGAGATAAACCCTGAAAGAGAGTGG 1741  
Db 1930 ATTTAGAAGAGAACTACATTCATGTTGTTGAGAGATAAACCCTGAAAGAGAGTGG 1989  
QY 1742 CTTATCTTTCACTTTATCGAAGTCAAGTGTATTTGTTTCATGTGTGATCAATTTTATATT 1801  
Db 1990 CTTATCTTTCACTTTATCGAAGTCAAGTGTATTTGTTTCATGTGTGATCAATTTTATATT 2049  
QY 1802 CTCCTTTGACATTAATGCTGTTTCTAACTCTGTTTAAATATATATCTATTTTACC 1861  
Db 2050 CTCCTTTGACATTAATGCTGTTTCTAACTCTGTTTAAATATATATCTATTTTACC 2109  
QY 1862 AAAGGTATTTAATATCTTTTTTATGACAACTTTAGATCAACTATTTTATGCTTGGTAAT 1921

Db 2110 AAAGGTATTTAATATCTTTTTTATGACAACTTAGATCAACTATTTTATGCTTGGTAAT 2169  
QY 1922 TTTTCTTAAACAAATGTTTATAGCCAGAGAAACAAAGATGGATATAAAAAATATTGTGCC 1981  
Db 2170 TTTTCTTAAACAAATGTTTATAGCCAGAGAAACAAAGATG---ATATAAAATATTGTGC 2226  
QY 1982 CTGGAACAAATACATGATATNTCCATCCCGAATCGTGTGCTAGAGTTGGAATTAACCTGCA 2041  
Db 2227 TCTGACAAATATACATGATATTT-CATCTCGTATGCTGTAGAGTTAGATT-AATCTGCA 2284  
QY 2042 TTTTAAAAAACCCTGAATTTGGGAAGGAANTTCGTAAGGTTGGCCAAANCTTTTTCAAAA 2101  
Db 2285 TTTTAAAAAACCCTGAATTT---GGAATAGAAATGCTGAAGTT---GCAAAAGACTTTTTCAAAA 2338  
QY 2102 TAAATTA 2108  
Db 2339 TAAATTA 2345

## RESULT 6

US-09-978-697-487  
; Sequence 487, Application US/09978697  
; Patent No. US20020169284A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC27  
; CURRENT APPLICATION NUMBER: US/09/978,697  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
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; PRIOR FILING DATE: 1998-03-11  
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; PRIOR FILING DATE: 1998-03-11

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 ; PRIOR FILING DATE: 1998-05-15  
 ;  
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 93.9%; Score 1979.4; DB 10; Length 2849;  
Best Local Similarity 97.7%; Pred. No. 0;  
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY	2	CCGCCGTGAGTGA	CTCTCACCCAGTCAGCCAAATAGAGCCTCTTCGGGCTTCTCTCTGG	61
Db	250	CCGCCGTGAGTGA	CTCTCACCCAGTCAGCCAAATAGAGCCTCTTCGGGCTTCTCTCTGG	309
QY	62	TGACATCTGCCCT	TGGCCGGCAGAGACGAGGACTCAGGCGGAATCAAACCTCAGTAGTA	121
Db	310	TGACATCTGCCCT	TGGCCGGCAGAGACGAGGACTCAGGCGGAATCAAACCTCAGTAGTA	369
QY	122	AATTCCAGTTTTT	CCAGCAAACAGAAACGAGTACAAGATCCTCAGCATGAGAGAA	181
Db	370	AATTCCAGTTTTT	CCAGCAAACAGAAACGAGTACAAGATCCTCAGCATGAGAGAA	429
QY	182	TTATTACTGTCTA	CTAATGGAAGTATCACAGCCCAAGGTTTCCTCATACTATCCAA	241
Db	430	TTATTACTGTCTA	CTAATGGAAGTATCACAGCCCAAGGTTTCCTCATACTATCCAA	489
QY	242	GAATAACGGTCT	TGGTATGGAGATTAGTACGATAGAGGAAAATGTATGATACAACCTTA	301
Db	490	GAATAACGGTCT	TGGTATGGAGATTAGTACGATAGAGGAAAATGTATGATACAACCTTA	549
QY	302	CGTTTGATGAAA	GAATTTGGGCTTGAAACCCAGAAGATGACATATGCAAGTATGATTTTG	361
Db	550	CGTTTGATGAAA	GAATTTGGGCTTGAAACCCAGAAGATGACATATGCAAGTATGATTTTG	609
QY	362	TAGAAGTTGAGG	ACCCAGTGATGGAACCTATATTAGGCGCTGGTGTTCTCGGTACTG	421
Db	610	TAGAAGTTGAGG	ACCCAGTGATGGAACCTATATTAGGCGCTGGTGTTCTCGGTACTG	669
QY	422	TACAGGAAACCA	GATTTCTTAAAGGAAATCAAATTTAGGATAAAGATTTGTATCTGATGAAT	481
Db	670	TACAGGAAACCA	GATTTCTTAAAGGAAATCAAATTTAGGATAAAGATTTGTATCTGATGAAT	729
QY	482	ATTTTCTCTTGA	ACCAAGGTTCTGATCCACATACAAATTTGATCATGCCCAATTTACAG	541
Db	730	ATTTTCTCTTGA	ACCAAGGTTCTGATCCACATACAAATTTGATCATGCCCAATTTACAG	789
QY	542	AAGCTGTGAGTC	CTTACAGTCCACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG	601
Db	790	AAGCTGTGAGTC	CTTACAGTCCACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG	849
QY	602	CTATAACTGCTTT	AGTACCTTGAAGACCTTATTCGATATCTTTGAACACGAGAGATGGC	661
Db	850	CTATAACTGCTTT	AGTACCTTGAAGACCTTATTCGATATCTTTGAACACGAGAGATGGC	909
QY	662	AGTTGGACTTTA	GAGATCTATATAGGCCAACTTGGGAACTTTTGGCAAGGCTTTTGTTT	721
Db	910	AGTTGGACTTTA	GAGATCTATATAGGCCAACTTGGGAACTTTTGGCAAGGCTTTTGTTT	969
QY	722	TTGGAAGAAAT	CCAGAGTGGTGAATCTGAACCTTTAAACAGAGGAGGTAAAGATTATACA	781
Db	970	TTGGAAGAAAT	CCAGAGTGGTGAATCTGAACCTTTAAACAGAGGAGGTAAAGATTATACA	1029
QY	782	GCTGCACACTCG	TAACTTCTCAGTGCCATAAGGGAAGAACTAAAGAGAACCGATACCA	841
Db	1030	GCTGCACACTCG	TAACTTCTCAGTGCCATAAGGGAAGAACTAAAGAGAACCGATACCA	1089
QY	842	TTTTTCTGGCC	AGGTTGTTCTCGTTTAAACGCTGTGTTGGGAACCTGTGCCCTTTGTCTCC	901
Db	1090	TTTTTCTGGCC	AGGTTGTTCTCGTTTAAACGCTGTGTTGGGAACCTGTGCCCTTTGTCTCC	1149
QY	902	ACAATTCGAAT	GTCAATGTGTCCTCAAGCAAAAGTTTACTTAAAAAATACCAAGAGTCC	961
Db	1150	ACAATTCGAAT	GTCAATGTGTCCTCAAGCAAAAGTTTACTTAAAAAATACCAAGAGTCC	1209
QY	962	TTCAGTTGAGAC	CAAGACCGGTTGTACAGGGGATTTGCAAAATCACTCACCGAGTGGCCC	1021

Db 2285 TTTTAAAAAAGTAATT---GCAATAGAATTGGTAAGTT---GCAAGAAGCTTTTGGAAAA 2338

Qy 2102 TAATTAA 2108

Db 2339 TAATTAA 2345

## RESULT 7

US-09-978-192A-487

; Sequence 487, Application US/09978192A

; Patent No. US20020177553A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C9

; CURRENT APPLICATION NUMBER: US/09/978,192A

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

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; PRIOR APPLICATION NUMBER: 60/077632

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; PRIOR APPLICATION NUMBER: 60/077641

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

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; PRIOR APPLICATION NUMBER: 60/078936

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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 93.9%; Score 1979.4; DB 10; Length 2849;  
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Qy 62 TGACATCTGCCCTGGCCGCCAGAGACGAGGACTCAGGCGGAATCCAACTGAGTAGTA 121

Db 310 TGACATCTGCCCTGGCCGCCAGAGACGAGGACTCAGGCGGAATCCAACTGAGTAGTA 369  
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## RESULT 8

US-09-999-832A-487

; Sequence 487, Application US/09999832A

; Publication No. US20020192706A1

; GENERAL INFORMATION:

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; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
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; APPLICANT: Fong, Sherman  
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; APPLICANT: Tumas, Daniel  
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; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC63  
; CURRENT APPLICATION NUMBER: US/09/999,832A  
; CURRENT FILING DATE: 2001-10-24  
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APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J  
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APPLICANT: Paoni, Nicholas F.  
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APPLICANT: Shelton, David L.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC7  
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CURRENT FILING DATE: 2001-10-15  
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Db 2110 AAAGGTATTTAATATCTTTTATGACAACTTAGATCAACTATTTTAGCTTGGTAAT 2169
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Db 2227 TCTGACAAAATACATGATATTT---CATCTCGATGTTGCTAGAGTTAGATT---AATCTGCA 2284
QY 2042 TTTTAAAAACCTGAAATTTGGGAANGAANTTGGTAAGTTGGCCAAANCTTTTGTGAAA 2101
Db 2285 TTTTAAAAACCTGAAAT---GGATAGAAATGTTGTAAGTT---GCAAGACTTTTGTGAAA 2338
QY 2102 TAAATTA 2108
Db 2339 TAAATTA 2345
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; Sequence 487, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 487
; LENGTH: 2849
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2715
; OTHER INFORMATION: unknown base
US-09-978-608A-487
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Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCCGCGGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG 61
Db 250 CCCGCGGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG 309
QY 62 TGACATCTGCCCTGCGCGCCAGAGACGAGGGAAGTCTCAGCGGAATCCAACTGAGTAGTA 121
Db 310 TGACATCTGCCCTGCGCGCCAGAGACGAGGGAAGTCTCAGCGGAATCCAACTGAGTAGTA 369
QY 122 AATTCAGTTTCCAGCAACAGGACAGAGCGGAGTCAAGATCTCTCAGCATGAGAGAA 181
Db 370 AATTCAGTTTCCAGCAACAGGACAGAGCGGAGTCAAGATCTCTCAGCATGAGAGAA 429
QY 182 TTATTACTCTGTCTACTAATGGAAGTATTACAGGCCCAAGGTTTCTCTACTATTATCCAA 241
Db 430 TTATTACTCTGTCTACTAATGGAAGTATTACAGGCCCAAGGTTTCTCTACTATTATCCAA 489
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Db 490 GAAATACGGTCTTGGTATGAGAGATTAGTAGCAGTAGAGAGAAATGTATGATACAACTTA 549
QY 302 CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 361
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QY 362 TAGAAGTTGAGAAACCCAGTGTGAAGTATATTAGGCGCTGCTGCTGTTCTGGTACTG 421
Db 610 TAGAAGTTGAGAAACCCAGTGTGAAGTATATTAGGCGCTGCTGCTGTTCTGGTACTG 669
QY 422 TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 481
Db 670 TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 729
QY 482 ATTTTCTCTTGAACACAGGTTCTGCATCCACTAGCAACATTTGTCAAGCCACATTTACAG 541
Db 730 ATTTTCTCTTGAACACAGGTTCTGCATCCACTAGCAACATTTGTCAAGCCACATTTACAG 789
QY 542 AAGCTGTGAGTCTCTCAGTGTCTACCCCTTACAGCTTTGCCACTTGGACCTGCTGCTAAATG 601
Db 790 AAGCTGTGAGTCTCTCAGTGTCTACCCCTTACAGCTTTGCCACTTGGACCTGCTGCTAAATG 849
QY 602 CTATAACCTGCTTTAGTACCTTTGGAGACCTTATTCGATATCTTTGAAACCAAGAGATGGC 661
Db 850 CTATAACCTGCTTTAGTACCTTTGGAGACCTTATTCGATATCTTTGAAACCAAGAGATGGC 909
QY 662 AGTTGGACTTAGAAGATCTATATAGCCCAACTTGGCACTTCTTGGCAAGGCTTTTGT 721
Db 910 AGTTGGACTTAGAAGATCTATATAGCCCAACTTGGCACTTCTTGGCAAGGCTTTTGT 969
QY 722 TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAAACAGAGAGGTAAGATTATACA 781
Db 970 TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAAACAGAGAGGTAAGATTATACA 1029
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782 GCTGCACACCTCGTAACCTCTCAGTGTCCATAGGGAAGAACTAAGAGAACCGATACCA 841  
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842 TTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGTGGGAACTGTGCTGTGTCTCC 901  
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962 TTCAGTTGAGACAAAGACCGGTGTGAGGGGATGACAAAATCACTCACCGACGTGGCCC 1021  
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1802 CTCCTTTTGCATTAATTAACCTGTTGGCTTTTCTAATCTTGTGTAAATATATCTATTTTACC 1861  
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Qy 2042 TTTTAAAAAACCTGTAATTTGGGAANGAANTTGGTAAGGTTGGCCAAANCTTTTTTCAAAA 2101  
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Qy 2102 TAATTAA 2108  
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RESULT 11

US-09-978-585A-487  
; Sequence 487, Application US/09978585A  
; Publication No. US20030049633A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
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; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC15  
; CURRENT APPLICATION NUMBER: US/09/978,585A  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 487  
; LENGTH: 2849  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 2715  
; OTHER INFORMATION: unknown base  
; US-09-978-585A-487

Query Match 93.9%; Score 1979.4; DB 11; Length 2849;  
Best Local Similarity 97.7%; Pred. No. 0;  
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

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QY 1330 ACCACGAGAGCTCTTGCCAGAGCTGTGCACTGCACTGCTGCTATTCTATTAGAGAACGT 1389  
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QY 2050 CTCTCTTTGACATTAATTAATCTGTTGGCTTTTCTAACTGTTTAAATATATCTATTTTACC 2109  
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RESULT 12



US-09-978-191A-487  
; Sequence 487, Application US/09978191A  
; Publication No. US20030050239A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C4  
; CURRENT APPLICATION NUMBER: US/09/978,191A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
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; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
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; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 93.9%; Score 1979.4; DB 11; Length 2849;  
Best Local Similarity 97.7%; Pred. No. 0;  
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Db 250 CCCCGCGTGTAGTCTCTACCCCGAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCTGC 309  
  
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Db 310 TGACATCTGCTTCCGCGGCGCAGAGACGAGGACTCTCAGGCGGAATCCAACTGAGTAGTA 369  
  
Qy 122 AATTCCAGTTTTCAGGCAACAGGAACAGACGAGGTACAGATCCCTCAGCATGAGAA 181  
Db 370 AATTCCAGTTTTCAGGCAACAGGAACAGACGAGGTACAGATCCCTCAGCATGAGAA 429  
  
Qy 182 TTATTACTGTCTACTAAATGGAAGTATTCACAGCCCAAGGTTTCTCTCATCTTATCAA 241

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Db 490 GAAATACCGTCTTGGTATGCGAGATTAGTAGCAGTAGAGAAAATGTATGGATCAACAATT 549  
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Db 550 CGTTTGATGAAAGATTTTGGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATGATTTG 609  
Qy 362 TAGAAGTTGAGRAACCCAGTGTGAACTATATATTAGGCGCTGGTGTGGTCTCGTACTG 421  
Db 610 TAGAAGTTGAGRAACCCAGTGTGAACTATATATTAGGCGCTGGTGTGGTCTCGTACTG 669  
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; Sequence 487, Application US/09978403A  
; Publication No. US20030050240A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherwan  
; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C17  
; CURRENT APPLICATION NUMBER: US/09/978,403A  
; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
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; PRIOR FILING DATE: 1998-03-31



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Db 1810 AGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAGAACTATGTTGCTATGAATTA 1869  
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Db 2110 AAAGGTATTTAAATATTTCTTTTATGACAACTTAGATCAACTATTTTATAGCTTGGTAAAT 2169  
Qy 1922 TTTTCTAAACAAATTTATAGCCAGAGAACAAAGATGGATATAAAATATTTGTTGCC 1981  
Db 2170 TTTTCTAAACAAATTTATAGCCAGAGAACAAAGATG---ATATAAATATTTGTTGCC 2226  
Qy 1982 CTGACAAAATACATGATNTCCATCCCGAATGCTGTAGAGTTGGATTTAAACCTGCA 2041  
Db 2227 TCTGACAAAATACATGATNT---CATCTCGTATGCTGTAGAGTTAGATT---AATCTGCA 2284  
Qy 2042 TTTTAAAAAACCTGAAATTTGGGAAGGAANTTGTAAAGTTGGCCCAANCTTTTGTGAAA 2101  
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Qy 2102 TAATTA 2108  
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RESULT 14  
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; Sequence 487, Application US/09978564A  
; Publication No. US20030050241A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker, Kevin P.  
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; APPLICANT: Desnoyers, Luc  
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; APPLICANT: Roy, Margaret Ann

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APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C25  
CURRENT FILING DATE: 2001-10-16  
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PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07





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Qy 1742 CCTTATCTTCACCTTATCGATAAGTCAGTTTATTTGTTTTCATTCGTGTACATTTTATATT 1801  
Db 1990 CCTTATCTTCACCTTATCGATAAGTCAGTTTATTTGTTTTCATTCGTGTACATTTTATATT 2049  
Qy 1802 CTCCTTTTGACATTAATCTGCTGCTTTCTTAATCTTGTGTTAAATATATCTATTTTACC 1861  
Db 2050 CTCCTTTTGACATTAATCTGCTGCTTTCTTAATCTTGTGTTAAATATATCTATTTTACC 2109  
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Db 2110 AAAGGTATTAATATCTTTTATGACAACTTAGATCAATATTTTAGCTTGGTAAAT 2169  
Qy 1922 TTTTCTAAACAACTTGTATAGCCAGAGGAAACAAAGATGATATAAAATATTTGTTGCC 1981  
Db 2170 TTTTCTAAACAACTTGTATAGCCAGAGGAAACAAAGATGATATAAAATATTTGTTGCC 2226  
Qy 1982 CTGACAAAATACATGTATTTCCATCCCGAATGGTCTAGAGTTGGATTAAACCTGCA 2041  
Db 2227 TCTGACAAAATACATGTATTT-CATTCTGATGGTCTAGAGTTAGATT-AACTGCA 2284  
Qy 2042 TTTTAAAAAAGCTGAATTTGGAAGGAATTTGGTAAGTTGGCCAAACCTTTTGTGAAA 2101  
Db 2285 TTTTAAAAAAGCTGAATTTGGAAGGAATTTGGTAAGTTG---GCAAGAGACTTTTGTGAAA 2338  
Qy 2102 TAATTA 2108  
Db 2339 TAATTA 2345

## RESULT 15

US-09-999-833A-487

; Sequence 487, Application US/09999833A

; Publication No. US20030054405A1

## ; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630FIC65

; CURRENT FILING DATE: 2001-10-24

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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

Qy      2      CCCGCCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG 61
Db      250     CCCGCCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGC 309

Qy      62      TGACATCTGCCCTGGCCGCCAGAGACGAGGAGCTCAGCGGAATCCAACTGAGTAGTA 121
Db      310     TGACATCTGCCCTGGCCGCCAGAGACGAGGAGCTCAGCGGAATCCAACTGAGTAGTA 369

Qy      122     AATCCAGTTTCCAGCAACAGGAACAGACGAGTCAAGATCCTCAGCATGAGAGAA 181
Db      370     AATCCAGTTTCCAGCAACAGGAACAGACGAGTCAAGATCCTCAGCATGAGAGAA 429

Qy      182     TTATTACTGTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTACTATATCCAA 241
Db      430     TTATTACTGTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTACTATATCCAA 489

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Qy      662     AGTGTGACTTAGAAGATCTATATAGCCCAACTTGGCAACTTCTTGGCAAGGCTTTTGT 721
Db      910     AGTGTGACTTAGAAGATCTATATAGCCCAACTTGGCAACTTCTTGGCAAGGCTTTTGT 969

Qy      722     TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTGAAGATTATACA 781
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Db	1030	GCTGCACACCTCGTAACCTCTCAGTGTCCATAAGGGGAAGAACTAAAGAGAACCGATACCA	1089		1922	TTTTCTAAACACAAATTTGTTATAGCCAGAGGAAACAAAGATGATATAAAAAATATTGTTGCC	1981
Qy	842	TTTTCTGGCCAGGTGTCTCCTGGTTAAACCGTGTGTGGGAACTGTGCGCTGTGTTCTCC	901		2170	TTTTCTAAACACAAATTTGTTATAGCCAGAGGAAACAAAGATG--ATATAAAATATTGTTGC	2226
Db	1090	TTTTCTGGCCAGGTGTCTCCTGGTTAAACCGTGTGTGGGAACTGTGCGCTGTGTTCTCC	1149		1982	CTGGACAAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTGCA	2041
Qy	902	ACAAATGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTTAAAAAAATACCACAGAGTCC	961		2227	TCTGACAAAAATACATGTATTT-CATTTCTGCTATGGTCTAGAGTTAGATT-AAATCTGCA	2284
Db	1150	ACAAATGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTTAAAAAAATACCACAGAGTCC	1209		2042	TTTTTAAAAAACCTCAATTGGGAANGGAANTTGGTAAGTTGGCCCAAAANTTTTTTGA AAA	2101
Qy	962	TTCAAGTTGAGACCAAGAACCGGTGTAGGGGATTTGCAAAATCACTCACCGAAGTGGCCC	1021		2285	TTTTTAAAAAACCTGAATT---GGAATAGAAATGGTAAAGTT---GCAAGAGACTTTTTTGA AAA	2338
Db	1210	TTCAAGTTGAGACCAAGAACCGGTGTAGGGGATTTGCAAAATCACTCACCGAAGTGGCCC	1269		2102	TAATTTAA	2108
Qy	1022	TGGAGCACCATGAGGAGTGTACTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGCATC	1081		2339	TAATTTAA	2345
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Qy	1442	TGCAAGTGAGCACCTGATTCGGTTGCCCTTGCTTAACCTCTAAAGCTCCATGTCTCGGCGCT	1501				
Db	1690	TGCAAGTGAGCACCTGATTCGGTTGCCCTTGCTTAACCTCTAAAGCTCCATGTCTCGGCGCT	1749				
Qy	1502	AAATCGTATAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTACATATGTAACC	1561				
Db	1750	AAATCGTATAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTACATATGTAACC	1809				
Qy	1562	AGAACATTTATGTAACAACTGGTTTTTAAAAAGGAACATAATGTTGCTATGAATTA	1621				
Db	1810	AGAACATTTATGTAACAACTGGTTTTTAAAAAGGAACATAATGTTGCTATGAATTA	1869				
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Db	1990	CCTTATCTTCATTTATCGTAAGTCAGTTTATTGTTTTCATTTGTGTACATTTTATATT	2049				
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Qy	1862	AAAGGTATTTAATATCTTTTATGACAACTTAGATCAACTATTTTAGCTTGGTAAAT	1921				

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 23:39:26 ; Search time 3075.92 Seconds  
(without alignments)  
16656.442 Million cell updates/sec

Title: US-09-852-209A-2

Perfect score: 2108

Sequence: 1 cccgcgcgtgagtgagctct.....nctttttgaaataattaa 2108

Scoring table:

IDENTITY\_NUC

Gapop 10\*0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

E8T:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hcc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hcc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1894.2	89.9	2826	11 BC041783	BC041783 Homo sapi
2	1892.4	89.8	2655	11 BC051876	BC051876 Homo sapi
3	960.2	45.6	3244	11 AK033734	AK033734 Mus muscu
4	959.4	45.5	2765	11 AK052947	AK052947 Mus muscu

5	957.8	45.4	3405	11	AK042767	AK042767 Mus muscu
6	891.4	42.3	2893	11	BC029099	BC029099 Mus muscu
7	834	39.6	999	13	BQ068266	BQ068266 AGENCOURT
8	796.2	37.8	969	10	BG677432	BG677432 602625259
9	768	36.4	811	10	BG185961	BG185961 RST4916 A
10	759.2	36.0	1142	10	BG681390	BG681390 602627750
11	733.4	34.8	802	12	B1870535	B1870535 603394005
12	697.2	33.1	769	14	CB309471	CB309471 AGENCOURT
13	641.6	30.4	686	12	BQ015321	BQ015321 UI-H-ED1-
14	631.8	30.0	2502	11	AK081347	AK081347 Mus muscu
15	608.2	28.9	789	12	B1911795	B1911795 603065222
16	572.8	27.2	631	10	AK958887	AK958887 EST370357
17	568.4	27.0	572	13	BQ694737	BQ694737 1000880 H
18	567.2	27.0	695	12	B1668022	B1668022 603295848
19	567.4	26.9	902	13	BUS17879	BUS17879 AGENCOURT
20	566.6	26.9	571	14	W63582	W63582 2b99b09.r1
21	560.6	26.6	567	12	BM827309	BM827309 K-E8T0099
22	559.4	26.5	696	10	BG430400	BG430400 602502113
23	548.8	26.0	574	14	CA397892	CA397892 cs97d11.y
24	540.4	25.6	835	10	BG681328	BG681328 602627178
25	534	25.3	771	14	CB310542	CB310542 AGENCOURT
26	533	25.3	780	10	BG681936	BG681936 602629877
27	505.4	24.0	715	10	BE879725	BE879725 601491625
28	499.2	23.7	562	9	AU280428	AU280428 AU280428
29	489.2	23.2	823	13	BUE14825	BUE14825 UI-M-EVO-
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31	482.2	22.9	523	10	BE958470	BE958470 601644787
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33	480.2	22.8	820	10	BF697294	BF697294 602129832
34	478.8	22.7	851	10	BF102859	BF102859 601646827
35	478.6	22.7	950	10	BF031624	BF031624 603558104
36	473.4	22.5	874	10	BF670092	BF670092 602119417
37	466.4	22.1	676	13	BU259419	BU259419 603415593
38	465.8	22.1	565	10	BE884591	BE884591 601506290
39	458.6	21.8	477	14	CB159806	CB159806 K-E8T0219
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41	444	21.1	556	10	BG609411	BG609411 323251.MA
42	434.2	20.6	983	10	BG112388	BG112388 602881957
43	433.6	20.6	889	10	BF698737	BF698737 602126283
44	432.4	20.5	886	10	BF217515	BF217515 601885209
45	432.2	20.5	877	10	BF137533	BF137533 601780532

#### ALIGNMENTS

RESULT 1	BC041783	2826 bp	mrna	linear	HTC 13-JAN-2003
LOCUS	BC041783	Homo sapiens, Similar to platelet-derived growth factor, C			
DEFINITION	BC041783	polypeptide, clone IMAGE:4614150, mRNA.			
ACCESSION	BC041783.1	GI:27692870			
VERSION	BC041783	HTC.			
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1	(bases 1 to 2826)			
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-DEC-2002) National Institutes of Health, Mammalian				
	Gene Collection (MGC), Cancer Genomics Office, National Cancer				
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,				
	USA				
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>				
COMMENT	Contact: MGC help desk				
	Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a>				
	Tissue Procurement: CLONTECH				
	cDNA Library Preparation: CLONTECH Laboratories, Inc.				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)				
	DNA Sequencing by: Sequencing Group at the Stanford Human Genome				
	Center, Stanford University School of Medicine, Stanford, CA 94305				

Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) mcd@axil.stanford.edu  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 41 Row: 9 Column: 9  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994186  
 This clone has the following problem: frame shifted.

## FEATURES

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 /clone="IMAGE:4614150"  
 /tissue\_type="Kidney"  
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 /lab\_host="DH10B"  
 /note="Vector: pDNR-LIB"  
 BASE COUNT 870 a 519 c 591 g 846 t

## ORIGIN

Query Match 89.9%; Score 1894.2; DB 11; Length 2826;  
 Best Local Similarity 94.8%; Pred. No. 5.6e-298;  
 Matches 2057; Conservative 1; Mismatches 38; Indels 73; Gaps 7;

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QY 2 CCGCGGTGAGTACCTCCACCCAGTCAGGCAATGAGCTCTCGGGCTTCCTGG 61
DB |||||
QY 62 TGACATCTGCCCTGCGCGCCAGAGACGAGGAGCTCAGCGGAATCCAACTGAGTAGTA 121
DB |||||
QY 249 TGACATCTGCCCTGCGCGCCAGAGACGAGGAGCTCAGCGGAATCCAACTGAGTAGTA 308
QY 122 AATTCAGTTTCCAGCAACAGGAACAGAAC----- 153
DB |||||
QY 309 AATTCAGTTTCCAGCAACAGGAACAGAACCGTAGGAACTATATCCAAGCATCTGGAC 368
QY 154 -----GGAGTACAAGATCCCTCAGCATGAGAGA 180
DB |||||
QY 369 TGGCATAGAAAGAGAGAGAAAGAACATTTAAAGAGATCAAGATCCTCAGCATGAGAGA 428
QY 181 ATTATTACTGTCTACTAATGGAAGTATTCAGGCCCAAGGTTTCCTCATACTTATCCA 240
DB |||||
QY 429 ATTATTACTGTCTACTAATGGAAGTATTCAGGCCCAAGGTTTCCTCATACTTATCCA 488
QY 241 AGAAATACGGTCTTGGTATGGAGATTAGTACGATAGAGGAAATGTATGGATACACTT 300
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QY 489 AGAAATACGGTCTTGGTATGGAGATTAGTACGATAGAGGAAATGTATGGATACACTT 548
QY 301 AGCTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTT 360
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QY 549 AGCTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTT 608
QY 361 GTAGAAGTTGAGAACCCAGTGAATGAACTATATTAGGCGCTGGTGGTCTGGTACT 420
DB |||||
QY 609 GTAGAAGTTGAGAACCCAGTGAATGAACTATATTAGGCGCTGGTGGTCTGGTACT 668
QY 421 GTACAGGAAACAGATTTCTAAAGGAATCAATTTAGGATGAATTTCTATCTGATGAA 480
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QY 669 GTACAGGAAACAGATTTCTAAAGGAATCAATTTAGGATGAATTTCTATCTGATGAA 728
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QY 729 TATTTTCCTCTGAACACGAGTTCTGCATCCACTCAACATTTGTCTATGCCAATTCACA 788
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DB |||||
QY 789 GAAGCTGTGAGTCTTTGAGTCTACCCCTTCAGCTTTGCGCACTGGACTGCTTAAATAT 848
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QY |||||
DB 721 TTTGGAAGAAATCCAGAGTGTGATCTGAACCTTTTAAACAGAGAGAGGTAAATATATAC 780
QY |||||
DB 969 TTTGGAAGAAATCCAGAGTGTGATCTGAACCTTTTAAACAGAGAGAGGTAAATATATAC 1028
QY |||||
DB 781 AGCTGCACACCTGTAACTTCTCAGTGTCCATAGGGAAGAACTTAAAGAGACCCATACC 840
QY |||||
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QY |||||
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QY |||||
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QY |||||
DB 901 CACAATTCGAATGAATGTCAATGTGTCCAAAGCAAAAGTTACTTAAAAAATACCAAGAGTGC 960
QY |||||
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1980	QY	CCCTGGCAAAATACATGTATNTCCATCCGGAAATGGTCTAGAGTTGATTAACACCTG	2039
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LOCUS	Homo sapiens cDNA clone IMAGE:6527736,			
DEFINITION	Homo sapiens cDNA clone IMAGE:6527736, containing frame-shift errors.			
ACCESSION	BC051876			
VERSION	BC051876.1	GI:30354290		
KEYWORDS	HTC.			
SOURCE	Homo sapiens (human)			

**ORGANISM**  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 2655)

**REFERENCE**  
AUTHORS  
Strausberg, R.L., Collins, F.S., Wagner, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Schenman, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,  
Carninci, P., Brange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shvachenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Krzywicki, M.I., Skalska, U., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Grigwold, J., Grimwood, J., Schmutz, J., Myers, R.M.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Warr, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences

JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)  
22388257  
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2 (bases 1 to 2655)  
Strausberg, R.  
Direct Submission  
Submitted (01-MAY-2003) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda MD 20892-2590,

REMARK	USA
COMMENT	<p>NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>          Contact: MGC help desk          Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a>          Tissue Procurement: ATCC          cDNA Library Preparation: Life Technologies, Inc.          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)          DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305          Web site: <a href="http://www-sbgc.stanford.edu">http://www-sbgc.stanford.edu</a>          Contact: (Dickson, Mark) <a href="mailto:mcdd@paxil.stanford.edu">mcdd@paxil.stanford.edu</a>          Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.</p>

Clone distribution: WGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 110 Row: p Column: 4  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994186  
This clone has the following problem: frame shifted

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FEATURES
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BASE COUNT
822 a 479 c 551 g 803 t

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Query Match	89.8%; Score 1892.4; DB 11; Length 2655;
Best Local Similarity	94.8%; Pred. No. 1.1e-297;
Matches 2056; Conservative	1; Mismatches 36; Indels 75; Gaps 7;
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Db	97 TGACATCTGCCCTGGCCGGCCAGAGACGAGGGAATCAGGGGGAATCCAACTCGAGTAGTA 156
Qy	122 AATTCCAGTTTTCCAGCAACAGGAAACAGAAC----- 153
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Qy	301 ACGTTTCATGAAGATTTGGCTTGAGACCCAGAAATGACATATCCAAAGTATGATTTT 360
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## RESULT 3

AK033734 3244 bp mRNA linear HTC 05-DEC-2002  
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ACCESSION AK033734.1 GI:26329432  
VERSION AK033734  
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SOURCE Mus musculus (house mouse)  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE 2  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
REFERENCE 3  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,



Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 20530913  
 11076861

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Functional annotation of a full-length mouse cDNA collection

#### REFERENCE

#### AUTHORS

Nature 409 (6821), 685-690 (2001)  
 21085660  
 11217851

#### REFERENCE

#### AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

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Nature 420, 563-573 (2002)  
 6 (bases 1 to 3244)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanaoka, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

#### REFERENCE

#### AUTHORS

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

#### COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/

#### FEATURES

#### source

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RESULT 4  
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DEFINITION  
Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D93001M08 product:platelet-derived growth factor, C polypeptide, full insert sequence.  
AK052947  
HTC; CAP trapper.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
2  
AUTHORS  
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AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE

AK052947 2765 bp mRNA linear HTC 05-DEC-2002  
Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D93001M08 product:platelet-derived growth factor, C polypeptide, full insert sequence.  
AK052947  
HTC; CAP trapper.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
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20499374  
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
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20530913  
11076861  
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# **TITLE**

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

21085660

11217851

5

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2765)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Oino, M., Ohsato, N.,

Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

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URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,

Fax: 81-45-503-9216)

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.go.jp/>

URL: <http://fantom.gsc.riken.go.jp/>.

Location/Qualifiers

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evidence: BLASTN, 99%, match=2691)

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polyA\_site 2765  
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Matches 1446; Conservative 1; Mismatches 578; Indels 31; Gaps 11;

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QY 122 AATTCAGTTTTCAGCAACAAGAACAGAGCAGGAGTACAGATCTCTCAGCATCAGAGAA 181  
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DB 479 GAAATATGGTGGTGGTGGAGATTAGTTCAGTAGATGAAATGTCGGATCCAGCTGA 538  
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LOCUS Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length  
DEFINITION enriched library, clone:A73002G11 product:platelet-derived growth  
factor, C polypeptide, full insert sequence.  
ACCESSION AK042767.1 GI:26335314  
VERSION HTC; CAP trapper.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1  
Carninci,P. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE 2  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20495574  
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REFERENCE 3  
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M.,  
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M.,  
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,  
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
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REFERENCE 4  
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,  
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Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,  
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Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,  
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,  
Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Buit,C.,  
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,  
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,  
Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,  
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,  
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Wyshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.  
and Hayashizaki,Y.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409 (6821), 685-690 (2001)



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RESULT 6  
LOCUS BC029099 2893 bp mRNA linear HTC 20-SEP-2002  
DEFINITION Mus musculus, similar to platelet-derived growth factor, C  
ACCESSION BC029099  
VERSION BC029099.1 GI:20809397  
KEYWORDS HTC.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 2893)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov  
COMMENT Contact: MGC help desk  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC  
Web site: http://www.hgsc.bcm.tmc.edu/cdna/  
Contact: amg@bcm.tmc.edu  
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Series: IRAP Plate: 35 Row: p Column: 20  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10242384  
This clone has the following problem: frame shifted.  
FEATURES  
Location/Qualifiers  
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Matches 1446; Conservative 1; Mismatches 578; Indels 89; Gaps 12;  
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Qy 1863 AAGTATTTAATAATCTTTTTTATGACAACCTAGATCAACTTATTTAGCTTGTGTAA--A 1920  
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Qy 1921 TTTTCTTAAACACAAATTTGTTATAGCCAGAGAAACAAGATG--GATATAAAATATATGT 1977  
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RESULT 7  
BQ068266

LOCUS DEFINITION BQ068266 999 bp mRNA linear EST 02-APR-2002  
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ACCESSION BQ068266  
VERSION BQ068266.1 GI:19897312  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 999)  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished  
JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Agencourt Bioscience Corporation



Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
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BASE COUNT 290 a 213 c 235 g 261 t  
ORIGIN

## FEATURES

source

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SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1. (bases 1 to 969)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgraphs-remail.nih.gov  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
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VERSION BG185961.1 GI:13707648
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini, Hominoidea; Homo.
REFERENCE 1 (bases 1 to 811)
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AUTHORS

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,  
Lerner, J., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,  
E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher,  
J., Danzig, J., and Ducar, M.

TITLE

Creation of genome-wide protein expression libraries using random

JOURNAL

Nat. Biotechnol. 19 (5), 440-445 (2001)

MEDLINE

21227151

PUBMED

11329013

COMMENT

Contact: Scott J. Cain

FEATURES

Location/Qualifiers

source

1. 811

BASE COUNT

225 a 172 c 195 g 216 t

ORIGIN

Query Match 36.4%; Score 768; DB 10; Length 811;

Best Local Similarity

97.8%; Pred. No. 5.4e-115;

Matches

788; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

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DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
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DB

DB 658 GTATTAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGATTTCCTAGCTGGGT 717

QY 1384 TCTGTATTTTCAGTCTTTTCGATACGCTTAGCGTAAATGTGCTAGTACAGGAAAAAAGTGTG 1443  
DB 718 TCTGTATTTTCAGTCTTTTCGATACGCTTA-GGTAAATGTCGTTACCGAAAAAAGTGTG 776

QY 1444 CAAAGTACGACCTGATTCGTTGCC 1468  
DB 777 CAAAGTACGACCTGATTCGTTGCC 801

RESULT 12  
CB309471  
LOCUS  
DEFINITION  
AGENCOURT 11834776 NICHDRh.Ov1 Macaca mulatta cDNA clone  
IMAGE:6893055 5', mRNA sequence.  
CB309471  
CB309471.1 GI:28832181  
EST.  
Macaca mulatta (rhesus monkey)  
ORGANISM  
Macaca mulatta  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecinae; Macaca.  
1 (bases 1 to 769)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-x@mail.nih.gov  
Tissue Procurement: Dr. Eliot Spindel  
cDNA Library Preparation: CLONTECH  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM3156 row: 1 column: 14  
High quality sequence stop: 590.  
Location/Qualifiers  
1. 769  
/organism="Macaca mulatta"  
/mol\_type="mRNA"  
/db\_xref="taxon:9544"  
/clone="IMAGE:6893055"  
/tissue\_type="Ovary"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NICHDRh.Ov1"  
/notes="Organ: ovary; Vector: pDNR-LIB; Site 1: Sfi I; Site 2: Sfi I; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.0-4.0 kb. Tissue pooled from pre-pubertal, post pubertal and menopausal monkeys. Constructed by Clontech. Note: this is a NICHDRh.Ov1 Library."  
BASE COUNT 220 a 158 c 188 g 202 t 1 others  
ORIGIN

Query Match 33.1%; Score 697.2; DB 14; Length 769;  
Best Local Similarity 96.0%; Pred. No. 1.7e-103;  
Matches 725; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 609 TGCCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACACGAGAGATAGGAGTGGGA 668  
DB 3 TGCCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACACGAGATAGGAGTGGGA 62

QY 669 CTTAGAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTGTTTGGGAAG 728  
DB 63 CTTAGAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTGTTTGGGAAG 122

QY 729 AAAATCCAGAGTGGTGGATCTGAACCTTCTAAACAGAGGAGGTAAAGATTATACAGCTGCAC 788  
DB 123 AAAATCCAGAGTGGTGGATCTGAACCTTCTAAACAGAGGAGGTAAAGATTATACAGCTGCAC 182

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QY 789 ACTCGTACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATACCAATTTCTG 848
Db 183 ACTCGTACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATACCAATTTCTG 242
QY 849 GCCAGTTTCTCTCTGGTTTAAACGCTGTGGTGGAACTGTGCTGTGCTTCCACAATTG 908
Db 243 GCCAGTTTCTCTCTGGTTTAAACGCTGTGGGAGGAACGTGCTGTGCTTCCACAATTG 302
QY 909 CAATGAATGTCAATGTGCTCCAGCAAAAGTTACTTAAATAATACCAAGAGTCTTCAAGTT 968
Db 303 CAATGAATGTCAATGTGCTCCAGCAAAAGTTACTTAAATAATACCAAGAGTCTTCAAGTT 362
QY 969 GAGACCAAAAGCCGGTGTGAGGGGATTCACAAATCACTCACCGAGTGGCCCTGGAGCA 1028
Db 363 GAGACCAAAAGCCGGTGTGAGGGGATTCACAAATCACTCACCGAGTGGCCCTGGAGCA 422
QY 1029 CCATGAGGAGTGTGCTGTGTCAGAGGAGACACAGGAGATAGCCGATCACCACCA 1088
Db 423 CCATGAGGAGTGTGCTGTGTCAGAGGAGACACAGGAGATAGCCGATCACCACCA 482
QY 1089 GCAGCTCTTGCACAGAGCTGTGCAGTGCAGTGCATCTATTAGAGAACGTATCGTT 1148
Db 483 GCAGCTCTTGCACAGAGCTGTGCAGTGCAGTGCATCTATTAGAGAACGTATCGTT 542
QY 1149 ATCTCCATCCTTAATCTCAGTGTGTTCTTCAAGGACCTTTCATCTTCAGGATTTACAGT 1208
Db 543 ATCTCCATCCTTAATCTCAGTGTGTTCTTCAAGGACCTTTCATCTTCAGGATTTACAGT 602
QY 1209 GCATTCGAAAGAGGAGACATCAACAGAAATAGGAGTTGTGCAACAGCTCTTTTGAGAG 1268
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QY 1269 GAGGCTTAAAGGACAGGAGAAAGGCTTCAATCGTGGAAAGAAATTTAAATGTTGATT 1328
Db 663 GAGGCTTAAAGGACAGGAGAAAGGCTTCAATCGTGGAAAGAAATTTAAATGTTGATT 722
QY 1329 AAATAGATCACCGAGTGTGTTT-CAGAGTTACCATG 1362
Db 723 AAATAGATCACCGAGTGTGTTT-CAGAGTTACCATG 757

RESULT 13
BQ015321/c
LOCUS
DEFINITION
  UT-H-ED1-axw-j-04-0-UI.s1 NCI CGAP_ED1 Homo sapiens cDNA clone
  IMAGE:5834595 3', mRNA sequence.
ACCESSION
  BQ015321
VERSION
  BQ015321.1 GI:19740222
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 686)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgaps-r@mail.nih.gov
  Tissue Procurement: Dr. Jose Mercuende
  cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Dr. M. Bento Soares, University of Iowa
  through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
  Seq primer: M13 FORWARD
  POLYA=Yes.
  Location/Qualifiers
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    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"

FEATURES
  source
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/clone="IMAGE:5834595"
/issue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_ED1"
/note="Organ: Left Pubic Bone; Vector: p773-Pac
(Pharmacia) with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCI CGAP ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C55. The library was constructed according to Bonaïdo
Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into p773-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_L1B=UI-H-ED1
TAG_TISSUE=chondrosarcoma
TAG_SEQ=CGTCAAGGCT"

BASE COUNT 197 a 152 c 130 g 207 t
ORIGIN

Query Match 30.4%; Score 641.6; DB 12; Length 686;
Best Local Similarity 98.8%; Pred. No. 1.9e-94;
Matches 666; Conservative 1; Mismatches 5; Indels 2; Gaps 2;

QY 974 CAAAGACCGGTGTGAGGGGATTCACAAATCACTCACCGAGTGGCCCTGGAGCACCATG 1033
Db 686 CAAAGACCGGTGTGCA-GGGATTGCAAAATCACTCACCGAGTGGCCCTGGAGCACCATG 628
QY 1034 AGCAGTGTGACTGTGTGCAGAGGAGACAGAGGATAGCCGATCACCACGAGCAGC 1093
Db 627 AGCAGTGTGACTGTGTGCAGAGGAGACAGAGGATAGCCGATCACCACGAGCAGC 568
QY 1094 TCTTGCCCGAGAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAACGATATGCGTTATCTC 1153
Db 567 TCTTGCCCGAGAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAACGATATGCGTTATCTC 508
QY 1154 CATCTTAAATCTCAGTGTGTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCAAT 1213
Db 507 CATCTTAAATCTCAGTGTGTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCAAT 448
QY 1214 CTGAAGAGGAGAGACATCAACAGAAATTTAGGAGTTGTGCAACAGCTCTTTTGGAGAGGAGC 1273
Db 447 TTGAAGAGGAGAGACATCAACAGAAATTTAGGAGTTGTGCAACAGCTCTTTTGGAGAGGAGC 388
QY 1274 CTAAAGGACAGGAGAAAGGCTTTCATCTGTGAAAGAAATTTAAATGTTGATATAATA 1333
Db 387 CTAAAGGACAGGAGAAAGGCTTTCATCTGTGAAAGAAATTTAAATGTTGATATAATA 328
QY 1334 GATCACCGAGTGTGTCAGAGTTACCATGTACGATTTCCACTAGCTGGGTTCTGTATTTC 1393
Db 327 GATCACCGAGTGTGTCAGAGTTACCATGTACGATTTCCACTAGCTGGGTTCTGTATTTC 268
QY 1394 AGTTCTTTTCGATACGGCTTAGGGTAAATGTGTCAGTACAGGAAAAAACTGTGCAAGTGAGCA 1453
Db 267 AGTTCTTTTCGATACGGCTTAGGGTAAATGTGTCAGTACAGGAAAAAACTGTGCAAGTGAGCA 208
QY 1454 CCTGATTCCGTTGCTTAACTCTAAAGCTCCATGTCTCTGGGCTTAAATCGTATAA 1513
Db 207 CCTGATTCCGTTGCTTAACTCTTAAAGCTCCATGTCTCTGGGCTTAAATCGTATAA 148
QY 1514 AATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTGTAACCGAGACATTTCTA 1572
Db 147 AATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTGTAACCGAGACATTTCTA 88
QY 1573 TGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAATTTAAATCTGTGCT 1632
Db 87 TGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAATTTAAATCTGTGCT 28
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:55:13 ; Search time 35.9375 Seconds  
(without alignments)  
1523.775 Million cell updates/sec

Title: US-09-852-209a-3  
Perfect score: 1858  
Sequence: 1 MSIFGLLVTSALAGQRGT.....DVALEHHECDVCVRGSGTG 345

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1858	100.0	345	21	AA1984557
2	1858	100.0	345	23	AA13212
3	1851	99.6	345	20	AA13679
4	1851	99.6	345	20	AA11766
5	1851	99.6	345	20	AA13023
6	1851	99.6	345	21	AA14857
7	1851	99.6	345	21	AA124250
8	1851	99.6	345	21	AA14322
9	1851	99.6	345	21	AA10633

10	1851	99.6	345	21	AA10635	Human VEGF-X prote
11	1851	99.6	345	21	AA10644	Human VEGF-X prote
12	1851	99.6	345	21	AA10650	Human 990126veg p
13	1851	99.6	345	21	AA10651	Human VEGF-X prote
14	1851	99.6	345	21	AA10657	Human VEGF-X prote
15	1851	99.6	345	21	AA10678	Human PRO200 (vasc
16	1851	99.6	345	21	AA10682	Human PRO200 prote
17	1851	99.6	345	21	AA10684	Human PRO1713 prote
18	1851	99.6	345	21	AA10685	Human TANGO 128.
19	1851	99.6	345	21	AA10688	Human growth facto
20	1851	99.6	345	21	AA10689	Bone morphogenic p
21	1851	99.6	345	22	AA10690	Human zveg3 polyp
22	1851	99.6	345	22	AA10691	Polypeptide for hu
23	1851	99.6	345	22	AA10692	Human PRO200 polyp
24	1851	99.6	345	22	AA10693	Human VEGF/PDGF-li
25	1851	99.6	345	22	AA10694	Human LP8, a PDGF-
26	1851	99.6	345	22	AA10695	Human zveg3 prote
27	1851	99.6	345	22	AA10696	Human PRO200 prote
28	1851	99.6	345	22	AA10697	Human angiogenesis
29	1851	99.6	345	23	AA10698	Human vascular end
30	1851	99.6	345	23	AA10699	Human VEGF-like pr
31	1851	99.6	345	23	AA10700	Human VEGF/PDGF-li
32	1851	99.6	345	23	AA10701	Human zveg3. Hom
33	1851	99.6	345	23	AA10702	Human zveg3 prote
34	1851	99.6	345	24	AA10703	Human growth facto
35	1851	99.6	345	24	AA10704	Human PRO polypept
36	1851	99.6	345	24	AA10705	Human secreted/tra
37	1851	99.6	345	24	AA10706	Novel secreted and
38	1851	99.6	345	24	AA10707	Human PRO200 polyp
39	1851	99.6	345	24	AA10708	Human vascular end
40	1851	99.6	345	21	AA10709	Human VEGF-X prote
41	1843	99.2	345	21	AA10710	Human VEGF-X homol
42	1843	99.2	345	21	AA10711	Human VEGF-X prote
43	1843	99.2	345	21	AA10712	Human growth facto
44	1745	93.9	354	21	AA10713	Human VEGF-X prote
45	1745	93.9	354	21	AA10714	Human VEGF-X prote

ALIGNMENTS

RESULT 1  
AA1984557  
ID AA1984557 standard; Protein; 345 AA.  
XX AC AA1984557;  
XX AC

DT 25-JUL-2000 (first entry)

DE Amino acid sequence of platelet-derived growth factor C (PDGF-C).

PA (UYHE-) UNIV HELSINKI LICENSING LTD.  
 XX Eriksson U, Aase K, Lee X, Ponten A, Uutela M, Alitalo K;  
 PI Oestman A, Heldin C, Betscholz C;  
 XX WPI; 2000-292954/25.  
 DR N-PSDB; AAA12523.  
 XX Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,  
 PT differentiation, growth and motility of cells expressing the PDGF-C  
 PT receptor -  
 XX Claim 27; Fig 2; 135pp; English.  
 PS  
 XX The present sequence represents human platelet-derived growth factor C  
 CC (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the  
 CC ability to stimulate and enhance proliferation or differentiation,  
 CC and/or growth or motility of cells expressing a PDGF-C receptor.  
 CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell  
 CC proliferation, preferably in combination with one other growth factor  
 CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also  
 CC be used for stimulating connective tissue or wound healing. The  
 CC PDGF-C polypeptide can be enzymatically processed to generate the active  
 CC truncated form of PDGF-C and used to regulate the receptor-binding  
 CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast  
 CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.  
 CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour  
 CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.  
 CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma  
 CC and erythroleukemia, can be identified by testing for expression of  
 CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue  
 CC remodelling during invasion of tumour cells into a normal population of  
 CC cells. Antagonists can also be used to treat fibrotic conditions,  
 CC especially found in the lung, kidney or liver.  
 XX  
 SQ Sequence 345 AA;

Query Match 100.0%; Score 1858; DB 21; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-179;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSFLGILLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
 Db 1 MSFLGILLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
 QY 61 PRPHTYPRNTVLVRLVAEENWVWLTDFERFGLDPEDDICKYDFVEVEEESDGTIL 120  
 Db 61 PRPHTYPRNTVLVRLVAEENWVWLTDFERFGLDPEDDICKYDFVEVEEESDGTIL 120  
 QY 121 GRWCGSTVPGKQISKGNQIRIRFVSDEYFPSPGFCIHYNIVMPQTEAVSPVLPSPA 180  
 Db 121 GRWCGSTVPGKQISKGNQIRIRFVSDEYFPSPGFCIHYNIVMPQTEAVSPVLPSPA 180  
 QY 181 LPDLNNATATSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVDNL 240  
 Db 181 LPDLNNATATSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVDNL 240  
 QY 241 LTBVRLYSCTPRNFVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECQCVPK 300  
 Db 241 LTBVRLYSCTPRNFVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECQCVPK 300  
 QY 301 VTKKYHEVLQRLPKTGVRLGKSLTDVALEHHEECDCVCRGSGTG 345  
 Db 301 VTKKYHEVLQRLPKTGVRLGKSLTDVALEHHEECDCVCRGSGTG 345

RESULT 2  
 AAEL13212  
 ID AAEL13212 standard; Protein; 345 AA.  
 XX  
 AC AAEL13212;  
 XX  
 DT 12-FEB-2002 (first entry)

XX Human platelet-derived growth factor (PDGF-C) protein.  
 DE  
 XX Human; transgenic animal; platelet derived growth factor C; PDGF-C;  
 KW cardiac hypertrophy; fibrosis.  
 XX Homo sapiens.  
 OS  
 XX WO200172132-A1.  
 EN  
 XX 04-OCT-2001.  
 PD  
 XX 28-MAR-2001; 2001WO-US09855.  
 PF  
 XX 28-MAR-2000; 2000US-192507P.  
 PR  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA Eriksson U, Li X, Ponten A, Aase K, Li H;  
 PI WPI; 2002-010700/01.  
 XX  
 XX A transgenic animal over-expressing platelet derived growth factor C is  
 PT useful to study and find therapy for disease associated with PDGF-C  
 PT over-expression, including cardiac hypertrophy and fibrosis -  
 XX Disclosure; Page 40-42; 48pp; English.  
 XX The patent discloses a method for producing a transgenic, non-human  
 CC animal over-expressing a platelet derived growth factor C (PDGF-C),  
 CC or its functional fragment or analogue. The method involves introducing  
 CC a transgenic PDGF-C DNA into a cell of a non-human animal, introducing  
 CC the cell into a non-human animal and allowing the cell to develop into  
 CC a transgenic, non-human animal. The transgenic animal is useful as a  
 CC model to study disease states characterised by over-expression of PDGF-C  
 CC and to find therapy for those diseases, particularly hypertrophy and  
 CC fibrosis in various organs including the heart. The present sequence  
 CC is PDGF-C protein from human.  
 XX  
 SQ Sequence 345 AA;

Query Match 100.0%; Score 1858; DB 23; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-179;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSFLGILLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
 Db 1 MSFLGILLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
 QY 61 PRPHTYPRNTVLVRLVAEENWVWLTDFERFGLDPEDDICKYDFVEVEEESDGTIL 120  
 Db 61 PRPHTYPRNTVLVRLVAEENWVWLTDFERFGLDPEDDICKYDFVEVEEESDGTIL 120  
 QY 121 GRWCGSTVPGKQISKGNQIRIRFVSDEYFPSPGFCIHYNIVMPQTEAVSPVLPSPA 180  
 Db 121 GRWCGSTVPGKQISKGNQIRIRFVSDEYFPSPGFCIHYNIVMPQTEAVSPVLPSPA 180  
 QY 181 LPDLNNATATSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVDNL 240  
 Db 181 LPDLNNATATSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVDNL 240  
 QY 241 LTBVRLYSCTPRNFVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECQCVPK 300  
 Db 241 LTBVRLYSCTPRNFVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECQCVPK 300  
 QY 301 VTKKYHEVLQRLPKTGVRLGKSLTDVALEHHEECDCVCRGSGTG 345  
 Db 301 VTKKYHEVLQRLPKTGVRLGKSLTDVALEHHEECDCVCRGSGTG 345

RESULT 3  
 AAY33679  
 ID AAY33679 standard; Protein; 345 AA.

XX AAY33679;  
XX 11-JAN-2000 (first entry)  
XX Human VEGF-E protein.  
XX VEGF-E; human; vascular endothelial cell growth factor; wound repair;  
XX treatment; cardiovascular disorder; endothelial disorder; therapy;  
XX tissue generation; regeneration; cardiac hypertrophy; cancer; detection;  
XX angiogenic disorder; age-related macular degeneration; vascular disease;  
XX neovascularization; tumor; gene mapping.  
XX  
XX Homo sapiens.  
XX WO9947677-A2.  
XX 23-SEP-1999.  
XX 10-MAR-1999; 99WO-US05190.  
XX 17-MAR-1998; 98US-0040220.  
XX 02-NOV-1998; 98US-0184216.  
XX (GETH ) GENENTECH INC.  
XX Ferrara N, Kuo SS;  
XX WPI; 1999-580306/49.  
XX N-PSDB; AA223691.  
XX New growth factor polypeptide useful for treating cardiovascular or  
XX endothelial disorders, e.g. cardiac hypertrophy -  
XX Claim 1; Fig 2; 122pp; English.  
XX This invention describes the isolation of a novel human vascular  
XX endothelial cell growth factor-E (VEGF-E) polypeptide which has  
XX tranquilizer, vulnery and cardiant activity. VEGF-E can be administered  
XX therapeutically, especially by expressing encoding polynucleotides, to  
XX treat cardiovascular or endothelial disorders in mammals, especially  
XX humans. It is useful in wound repair and tissue generation and  
XX regeneration, and may especially be used to treat cardiac hypertrophy  
XX It can be combined with a carrier in pharmaceutical compositions, which  
XX can be administered to treat disorders as above. VEGF-E can be used to  
XX screen for antagonists and agonists, and the antagonists administered to  
XX treat angiogenic disorders in mammals (especially humans) e.g. cancer or  
XX age-related macular degeneration. It can be used to generate antibodies,  
XX useful therapeutically as antagonists, as above. The antibodies are also  
XX useful to detect VEGF-E polypeptide, especially to diagnose  
XX cardiovascular, endothelial or angiogenic disorders in mammals (e.g.  
XX vascular disease, or neovascularization associated with tumor formation),  
XX by contacting the antibody with a tissue sample and detecting formation  
XX of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding  
XX VEGF-E can be used to diagnose cardiovascular and endothelial disorders  
XX in mammals, by detecting abnormally high or low VEGF-E gene expression in  
XX tissue samples. They can also be used to diagnose a disease or  
XX susceptibility to a disease related to a mutated form of VEGF-E (e.g. a  
XX cardiovascular, endothelial or angiogenic disorder such as a tumor), by  
XX detecting a mutation in the VEGF-E-encoding sequence isolated from a  
XX sample. They may also be used to produce probes useful to detect related  
XX sequences or for gene mapping. This sequence represents the human VEGF-E  
XX protein described in the method of the invention.  
XX Sequence 345 AA;  
XX Query Match 99.6%; Score 1851; DB 20; Length 345;  
XX Best Local Similarity 99.4%; Pred. No. 7e-179;  
XX Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MSLFGLLLVTSALAGQRRGTQAENLSKGFQSSNKEQNGVDPQHERIITVSTNGSIHS 60  
Db 1 MSLFGLLLVTSALAGQRRGTQAENLSKGFQSSNKEQNGVDPQHERIITVSTNGSIHS 60

QY 61 PRFPHTYPRNTVLVRLVAEENWVLIQLTFDERFGLDEPDDICKYDFVEVERPSDCTIL 120  
DB 61 PRFPHTYPRNTVLVRLVAEENWVLIQLTFDERFGLDEPDDICKYDFVEVERPSDCTIL 120  
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPPSPGFCIHNYIYMPQFTEAVSPSVLPSPA 180  
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPPSPGFCIHNYIYMPQFTEAVSPSVLPSPA 180  
QY 181 LPDLIANNAITAFSTLEDLIRVLEPERWOLDLEDLYRPTWOLLGKAFVFGKRSRVVDNL 240  
DB 181 LPDLIANNAITAFSTLEDLIRVLEPERWOLDLEDLYRPTWOLLGKAFVFGKRSRVVDNL 240  
QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPCLLVKRCGNACCLHNCNCCQCVPSK 300  
DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPCLLVKRCGNACCLHNCNCCQCVPSK 300  
QY 301 VTKKXHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345  
DB 301 VTKKXHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345  
RESULT 4  
ID AAY41766 standard; Protein; 345 AA.  
XX AC AAY41766;  
XX 07-DEC-1999 (first entry)  
XX Human PRO200 protein sequence.  
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
XX probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
XX secreted protein; transmembrane protein.  
XX Homo sapiens.  
XX WO9946281-A2.  
XX 16-SEP-1999.  
XX 08-MAR-1999; 99WO-US05028.  
XX 10-MAR-1998; 98US-0077450.  
XX 11-MAR-1998; 98US-0077632.  
XX 11-MAR-1998; 98US-0077641.  
XX 11-MAR-1998; 98US-0077649.  
XX 12-MAR-1998; 98US-0077791.  
XX 13-MAR-1998; 98US-0078004.  
XX 17-MAR-1998; 98US-0040220.  
XX 20-MAR-1998; 98US-0078886.  
XX 20-MAR-1998; 98US-0078910.  
XX 20-MAR-1998; 98US-0078936.  
XX 25-MAR-1998; 98US-0078939.  
XX 26-MAR-1998; 98US-0079294.  
XX 27-MAR-1998; 98US-0079656.  
XX 27-MAR-1998; 98US-0079663.  
XX 27-MAR-1998; 98US-0079664.  
XX 27-MAR-1998; 98US-0079689.  
XX 27-MAR-1998; 98US-0079728.  
XX 30-MAR-1998; 98US-0079786.  
XX 30-MAR-1998; 98US-0079920.  
XX 31-MAR-1998; 98US-0079923.  
XX 31-MAR-1998; 98US-0080105.  
XX 31-MAR-1998; 98US-0080107.  
XX 31-MAR-1998; 98US-0080165.  
XX 01-APR-1998; 98US-0080194.  
XX 01-APR-1998; 98US-0080327.  
XX 01-APR-1998; 98US-0080328.  
XX 01-APR-1998; 98US-0080333.  
XX 01-APR-1998; 98US-0080334.  
XX 08-APR-1998; 98US-0081049.

PR 08-APR-1998; 98US-0081070.  
PR 08-APR-1998; 98US-0081071.  
PR 09-APR-1998; 98US-0081195.  
PR 09-APR-1998; 98US-0081203.  
PR 09-APR-1998; 98US-0081229.  
PR 15-APR-1998; 98US-0081817.  
PR 15-APR-1998; 98US-0081838.  
PR 15-APR-1998; 98US-0081952.  
PR 15-APR-1998; 98US-0081955.  
PR 21-APR-1998; 98US-0082568.  
PR 21-APR-1998; 98US-0082569.  
PR 22-APR-1998; 98US-0082700.  
PR 22-APR-1998; 98US-0082704.  
PR 22-APR-1998; 98US-0082804.  
PR 23-APR-1998; 98US-0082767.  
PR 23-APR-1998; 98US-0082796.  
PR 27-APR-1998; 98US-0083336.  
PR 28-APR-1998; 98US-0083322.  
PR 29-APR-1998; 98US-0083392.  
PR 29-APR-1998; 98US-0083495.  
PR 29-APR-1998; 98US-0083496.  
PR 29-APR-1998; 98US-0083499.  
PR 29-APR-1998; 98US-0083500.  
PR 29-APR-1998; 98US-0083545.  
PR 29-APR-1998; 98US-0083554.  
PR 29-APR-1998; 98US-0083558.  
PR 29-APR-1998; 98US-0083559.  
PR 30-APR-1998; 98US-0083742.  
PR 05-MAY-1998; 98US-0084366.  
PR 06-MAY-1998; 98US-0084414.  
PR 06-MAY-1998; 98US-0084441.  
PR 07-MAY-1998; 98US-0084598.  
PR 07-MAY-1998; 98US-0084600.  
PR 07-MAY-1998; 98US-0084627.  
PR 07-MAY-1998; 98US-0084837.  
PR 07-MAY-1998; 98US-0084839.  
PR 07-MAY-1998; 98US-0084840.  
PR 07-MAY-1998; 98US-0084843.  
PR 13-MAY-1998; 98US-0085323.  
PR 13-MAY-1998; 98US-0085338.  
PR 13-MAY-1998; 98US-0085339.  
PR 15-MAY-1998; 98US-0085573.  
PR 15-MAY-1998; 98US-0085579.  
PR 15-MAY-1998; 98US-0085580.  
PR 15-MAY-1998; 98US-0085582.  
PR 15-MAY-1998; 98US-0085689.  
PR 15-MAY-1998; 98US-0085697.  
PR 15-MAY-1998; 98US-0085700.  
PR 15-MAY-1998; 98US-0085704.  
PR 18-MAY-1998; 98US-0086023.  
PR 22-MAY-1998; 98US-0086392.  
PR 22-MAY-1998; 98US-0086414.  
PR 22-MAY-1998; 98US-0086430.  
PR 22-MAY-1998; 98US-0086486.  
PR 28-MAY-1998; 98US-0087098.  
PR 28-MAY-1998; 98US-0087106.  
PR 28-MAY-1998; 98US-0087208.  
PR 30-JUL-1998; 98US-0094651.  
PR 11-SEP-1998; 98US-0100038.  
PA (GETH ) GENENTECH INC.  
XX  
XX  
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
XX  
XX WPI; 1999-551358/46.  
XX N-PSDB; AA234296.  
XX  
XX New secreted and transmembrane polypeptides and their polynucleotides,  
PT useful for treating blood coagulation disorders, cancers and cellular  
PT adhesion disorders -  
XX  
XX Claim 12; Fig 207; 530pp; English.  
PS  
XX

CC The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as  
CC sources of probes, primers, for chromosome mapping, and for generation  
CC of antisense sequences. They can also be used to create transgenic  
CC animals. The proteins can be used to treat a variety of diseases and  
CC disorders, depending on their function. Diseases that may be treated  
CC include blood coagulation disorders, cancers and cellular adhesion  
CC disorders. They may also be used to raise antibodies. AA233891 to  
CC AA234338, and AA41685 to AA41774 represent polynucleotide and  
CC polypeptide sequence given in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 345 AA;  
Query Match 99.6%; Score 1851; DB 20; Length 345;  
Best Local Similarity 99.4%; Pred. No. 7e-179;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSLFGLLLVTSALAGORRGTAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
DB 1 MSLFGLLLVTSALAGORRGTAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
QY 61 PRPPTYPRNTVLVWRLVAEENVMVQLTFDERFGLDEDDICKYDFVEVEPSDGTIL 120  
DB 61 PRPPTYPRNTVLVWRLVAEENVMVQLTFDERFGLDEDDICKYDFVEVEPSDGTIL 120  
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFEPSEPGFCIHYNIVMPQTEAVSVLPSPA 180  
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFEPSEPGFCIHYNIVMPQTEAVSVLPSPA 180  
QY 181 LPDLNLNNAITAPSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDNL 240  
DB 181 LPDLNLNNAITAPSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDNL 240  
QY 241 LTEEVRLYSCTPRNFSVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQCVPSK 300  
DB 241 LTEEVRLYSCTPRNFSVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQCVPSK 300  
QY 301 VTKKYHEVLQRLPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345  
DB 301 VTKKYHEVLQRLPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345  
RESULT 5  
AA230023  
ID AA230023 standard; Protein; 345 AA.  
XX  
XX AA230023;  
XX  
XX 11-OCT-1999 (first entry)  
XX Human vascular endothelial growth factor related protein.  
XX  
XX Vascular endothelial growth factor related protein; VEGF-R protein;  
KW tissue growth inhibition; tumour growth; cancer; tissue growth;  
KW angiogenesis; coronary artery blockage.  
XX  
XX Homo sapiens.  
XX  
XX WO9937671-A1.  
XX  
XX 29-JUL-1999.  
XX  
XX 26-JAN-1999; 99WO-US01574.  
XX  
XX 31-AUG-1998; 98US-0098548.  
PR 27-JAN-1998; 98US-0072635.  
PR 05-JUN-1998; 98US-0080809.  
PR 24-JUN-1998; 98US-0090544.  
XX  
XX (ELIL ) LILLY & CO ELI.  
XX  
XX Dou S, Na S, Song HY;

XX	PF	03-MAY-2000; 2000WO-US40047.	XX	PF	03-MAY-2000; 2000WO-US40047.
XX	PR	03-MAY-1999; 99US-0304216.	XX	PR	03-MAY-1999; 99US-0304216.
XX	PR	10-NOV-1999; 99US-016463.	XX	PR	10-NOV-1999; 99US-016463.
XX	PR	04-FEB-2000; 2000US-0180169.	XX	PR	04-FEB-2000; 2000US-0180169.
XX	PA	(ZYMO) ZYMOGENETICS INC.	XX	PA	(ZYMO) ZYMOGENETICS INC.
XX	PI	Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;	XX	PI	Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
XX	WI	WI; 2000-687541/67.	XX	WI	WI; 2000-687541/67.
XX	DR	N-PSDB; AAC81582.	XX	DR	N-PSDB; AAC81582.
XX	PT	Growth factor homologs and the nucleic acids that encode them, useful e.g. for treating liver damage, ischemia, multiple sclerosis and Alzheimer's disease -	XX	PT	Growth factor homologs and the nucleic acids that encode them, useful e.g. for treating liver damage, ischemia, multiple sclerosis and Alzheimer's disease -
XX	PS	Claim 48; Page 125-126; 143pp; English.	XX	PS	Claim 48; Page 125-126; 143pp; English.
XX	CC	The invention relates to the human growth factor homologue zvegfg4 (AAB48653), and nucleic acids encoding it (AAC81555). Zvegfg4 is a member of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial growth factor) family. Zvegfg4 has a growth factor domain (AAB48654) characterised by a PDGF cysteine knot structure, and a CUB domain (AAB48655) which has a beta barrel structure. Zvegfg4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3 fusions; expression constructs and host cells comprising human zvegfg3 nucleic acids; the recombinant expression of human zvegfg4; an antibody which binds to human zvegfg4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a method of modulating the proliferation, differentiation, migration or metabolism of bone cells, comprising exposing bone cells to zvegfg4-derived polypeptides; and a method of detecting a genetic abnormality in the zvegfg4 gene of a patient. Zvegfg4 proteins and derived fragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may be used in the treatment of periodontal disease and fractures. They may also be used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents human zvegfg3.	XX	CC	The invention relates to the human growth factor homologue zvegfg4 (AAB48653), and nucleic acids encoding it (AAC81555). Zvegfg4 is a member of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial growth factor) family. Zvegfg4 has a growth factor domain (AAB48654) characterised by a PDGF cysteine knot structure, and a CUB domain (AAB48655) which has a beta barrel structure. Zvegfg4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3 fusions; expression constructs and host cells comprising human zvegfg3 nucleic acids; the recombinant expression of human zvegfg4; an antibody which binds to human zvegfg4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a method of modulating the proliferation, differentiation, migration or metabolism of bone cells, comprising exposing bone cells to zvegfg4-derived polypeptides; and a method of detecting a genetic abnormality in the zvegfg4 gene of a patient. Zvegfg4 proteins and derived fragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may be used in the treatment of periodontal disease and fractures. They may also be used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents human zvegfg3.
XX	SQ	Sequence 345 AA;	XX	SQ	Sequence 345 AA;
XX	Query Match	99.6%; Score 1851; DB 21; Length 345;	XX	Query Match	99.6%; Score 1851; DB 21; Length 345;
XX	Best Local Similarity	99.4%; Pred. No. 7e-179;	XX	Best Local Similarity	99.4%; Pred. No. 7e-179;
XX	Matches 343; Conservative	2; Mismatches 0; Indels 0; Gaps 0;	XX	Matches 343; Conservative	2; Mismatches 0; Indels 0; Gaps 0;
QY	1	MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVDPQHERIITVSTNGSIHS 60	QY	1	MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVDPQHERIITVSTNGSIHS 60
DB	1	MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVDPQHERIITVSTNGSIHS 60	DB	1	MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVDPQHERIITVSTNGSIHS 60
QY	61	PRPHTYPRNTVLVRLVAEENVMQLTDFRFGLEDPEDDICKYDFVEVEEPESDGTIL 120	QY	61	PRPHTYPRNTVLVRLVAEENVMQLTDFRFGLEDPEDDICKYDFVEVEEPESDGTIL 120
DB	61	PRPHTYPRNTVLVRLVAEENVMQLTDFRFGLEDPEDDICKYDFVEVEEPESDGTIL 120	DB	61	PRPHTYPRNTVLVRLVAEENVMQLTDFRFGLEDPEDDICKYDFVEVEEPESDGTIL 120
QY	121	GRWCGSGTVPGKQISKGNQIRIRFVSDYFFPSPGFCIHYNIVMPQFTEAVSPVLPPSA 180	QY	121	GRWCGSGTVPGKQISKGNQIRIRFVSDYFFPSPGFCIHYNIVMPQFTEAVSPVLPPSA 180
DB	121	GRWCGSGTVPGKQISKGNQIRIRFVSDYFFPSPGFCIHYNIVMPQFTEAVSPVLPPSA 180	DB	121	GRWCGSGTVPGKQISKGNQIRIRFVSDYFFPSPGFCIHYNIVMPQFTEAVSPVLPPSA 180
QY	181	LPDLLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWQLLKAFFVGRKSRVVDLNL 240	QY	181	LPDLLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWQLLKAFFVGRKSRVVDLNL 240
DB	181	LPDLLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWQLLKAFFVGRKSRVVDLNL 240	DB	181	LPDLLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWQLLKAFFVGRKSRVVDLNL 240
QY	241	LTEEVRVLYCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300	QY	241	LTEEVRVLYCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
DB	241	LTEEVRVLYCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300	DB	241	LTEEVRVLYCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
QY	301	VTKKYHEVLQRLPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345	QY	301	VTKKYHEVLQRLPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345
DB	301	VTKKYHEVLQRLPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345	DB	301	VTKKYHEVLQRLPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345
XX	RESULT 6		XX	RESULT 6	
XX	AAB48657		XX	AAB48657	
XX	ID	AAB48657 standard; Protein; 345 AA.	XX	ID	AAB48657 standard; Protein; 345 AA.
XX	AC	AAB48657;	XX	AC	AAB48657;
XX	DT	09-MAR-2001 (first entry)	XX	DT	09-MAR-2001 (first entry)
XX	DE	Human zvegfg3, SEQ ID NO:33.	XX	DE	Human zvegfg3, SEQ ID NO:33.
XX	KW	Human; zvegfg3; zvegfg4 fusion; growth factor homologue; VEGF/PDGF family; CUB domain; PDGF-like activity; mitogenic; osteogenic;	XX	KW	Human; zvegfg3; zvegfg4 fusion; growth factor homologue; VEGF/PDGF family; CUB domain; PDGF-like activity; mitogenic; osteogenic;
XX	KW	neovascularisation; tissue repair; proliferation; differentiation; liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis; periodontal disease; bone fracture; wound healing; vulnarary; ischaemia; immunomodulation; hepatic.	XX	KW	neovascularisation; tissue repair; proliferation; differentiation; liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis; periodontal disease; bone fracture; wound healing; vulnarary; ischaemia; immunomodulation; hepatic.
XX	OS	Homo sapiens.	XX	OS	Homo sapiens.
XX	PN	WO20006736-A1.	XX	PN	WO





CC activity. The polynucleotides and polypeptides can be used for detecting  
 CC the presence of PRO polypeptides in samples, for linking bioactive  
 CC molecules to cells and for modulating biological activities of cells,  
 CC using the polypeptides for specific targeting. The polypeptide targeting  
 CC can be used to kill the target cells, e.g. for the treatment of cancers.  
 CC The polypeptide pairs provide specific targeting of bioactive molecules  
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
 CC the isolation of the PRO polynucleotide sequences.

XX Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 21; Length 345;  
 Best Local Similarity 99.4%; Pred. No. 7e-179;  
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFGLLLVTSALAGQRGTQAESNLSSKFQSSNKEQNGVQDPOHERIITVSTNGSIHS 60  
 Db 1 MSFGLLLVTSALAGQRGTQAESNLSSKFQSSNKEQNGVQDPOHERIITVSTNGSIHS 60

Qy 61 PRFHTYPRNTLVWRLVAEENWVQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120  
 Db 61 PRFHTYPRNTLVWRLVAEENWVQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120

Qy 121 GRWCGSGTVFGKQISKGNQIRIRFVSDYFPEFGFCIHYNVMPQFTEAVSPVLPPSA 180  
 Db 121 GRWCGSGTVFGKQISKGNQIRIRFVSDYFPEFGFCIHYNVMPQFTEAVSPVLPPSA 180

Qy 181 LPDLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWLLGKAFVFGKRSRVVDLNL 240  
 Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWLLGKAFVFGKRSRVVDLNL 240

Qy 241 LTBVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300  
 Db 241 LTBVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300

Qy 301 VTKYHEVLQRPKTGVRGLHKSITDVALEHHEEDCVCGRSTGG 345  
 Db 301 VTKYHEVLQRPKTGVRGLHKSITDVALEHHEEDCVCGRSTGG 345

RESULT 9

AAB10633  
 ID AAB10633 standard; Protein; 345 AA.

XX AAB10633;

XX 19-JAN-2001 (first entry)

XX Human RACE generated VEGF-X protein.

XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;  
 XX anti-rheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;  
 XX angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
 XX rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
 XX tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
 XX venous sore; diabetic ulcer; burns; skin graft growth.

OS Homo sapiens.

XX WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US30503.

XX 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX (JANC ) JANSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiowska A;

PI Dhanaraj SN, Xu J;

XX

DR WPI; 2000-442669/38.

XX N-PSDB; AAA71951.

XX New vascular endothelial growth factor protein, useful for treating or  
 PT preventing diseases associated with inappropriate angiogenesis activity  
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX Disclosure; Fig 6; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X  
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has  
 CC vulnary, cytostatic, anti-rheumatic, antiarthritic, antipsoriatic and  
 CC anti-diabetic activity and acts as an angiogenesis and vascularization  
 CC regulator. An antisense molecule of the invention is useful for treating  
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
 CC retinopathy by inhibiting angiogenic activity or inappropriate  
 CC vascularization including formation and proliferation of new blood  
 CC vessels, growth and development of tissues, tissue regeneration and organ  
 CC and tissue repair in a subject. The products of the invention are useful  
 CC for preparing medicaments for treating wounds such as dermal ulcers,  
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
 CC skin graft growth, tissue repair, proliferation of new blood vessels,  
 CC tissue regeneration and organ repair by promoting angiogenic activity or  
 CC vascularization. This sequence represents the RACE generated human VEGF-X  
 CC protein described in the method of the invention.

XX Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 21; Length 345;  
 Best Local Similarity 99.4%; Pred. No. 7e-179;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFGLLLVTSALAGQRGTQAESNLSSKFQSSNKEQNGVQDPOHERIITVSTNGSIHS 60

Db 1 MSFGLLLVTSALAGQRGTQAESNLSSKFQSSNKEQNGVQDPOHERIITVSTNGSIHS 60

Qy 61 PRFHTYPRNTLVWRLVAEENWVQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120

Db 61 PRFHTYPRNTLVWRLVAEENWVQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120

Qy 121 GRWCGSGTVFGKQISKGNQIRIRFVSDYFPEFGFCIHYNVMPQFTEAVSPVLPPSA 180

Db 121 GRWCGSGTVFGKQISKGNQIRIRFVSDYFPEFGFCIHYNVMPQFTEAVSPVLPPSA 180

Qy 181 LPDLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWLLGKAFVFGKRSRVVDLNL 240

Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWLLGKAFVFGKRSRVVDLNL 240

Qy 241 LTBVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300

Db 241 LTBVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300

Qy 301 VTKYHEVLQRPKTGVRGLHKSITDVALEHHEEDCVCGRSTGG 345

Db 301 VTKYHEVLQRPKTGVRGLHKSITDVALEHHEEDCVCGRSTGG 345

RESULT 10

AAB10635

ID AAB10635 standard; Protein; 345 AA.

XX AAB10635;

XX 19-JAN-2001 (first entry)

XX Human VEGF-X protein #1 isolated from clones 4 and 7.

XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;  
 XX anti-rheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;  
 XX angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
 XX rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
 XX tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;

```
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US30503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
PA (JANC ) JANSSEN PHARM NV.
XX
PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI; 2000-442669/38.
DR N-PSDB; AAA71955.
XX
XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
PS Disclosure; Fig 9; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antiangiogenic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC isolated from clones 4 and 7 described in the method of the invention.
XX
SQ Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 21; Length 345;
Best Local Similarity 99.4%; Pred. No. 7e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGORRGQTQAESNLSSKFFQSSNKEQNGVQDPQHERITVTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGQTQAESNLSSKFFQSSNKEQNGVQDPQHERITVTNGSIHS 60
QY 61 PRPHPTVPRNTVLVWLVAVENNVQLTDFRFGLEDDEDDICKYDFVEVEPSPDGTL 120
Db 61 PRPHPTVPRNTVLVWLVAVENNVQLTDFRFGLEDDEDDICKYDFVEVEPSPDGTL 120
QY 121 GRWCGSGTVPGKQISGNQIRIRFVSDPEYPPSPGFCIHYNIVMPQFTAVSPSVLPSPA 180
Db 121 GRWCGSGTVPGKQISGNQIRIRFVSDPEYPPSPGFCIHYNIVMPQFTAVSPSVLPSPA 180
QY 181 LPDLNLNNAITAFSTLLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLNLNNAITAFSTLLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
QY 241 LTEEVLVYSCTPNFVSIFREELKRTDTIPWPGCLLVKRCGNCACCLHNCNCQCVPFSK 300
Db 241 LTEEVLVYSCTPNFVSIFREELKRTDTIPWPGCLLVKRCGNCACCLHNCNCQCVPFSK 300
QY 301 VTKKYHEVLQRLPKTGVGRGLHKSITDVALEHHECDVCVCRGSTGG 345
Db 301 VTKKYHEVLQRLPKTGVGRGLHKSITDVALEHHECDVCVCRGSTGG 345
```

```
Db 301 VTKKYHEVLQRLPKTGVGRGLHKSITDVALEHHECDVCVCRGSTGG 345
RESULT 11
AAB10644
ID AAB10644 standard; Protein; 345 AA.
XX
AC AAB10644;
XX
DT 19-JAN-2001 (first entry)
XX
DE Human VEGF-X protein #4.
XX
XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antiangiogenic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US30503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
PA (JANC ) JANSSEN PHARM NV.
XX
PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI; 2000-442669/38.
DR N-PSDB; AAA71990.
XX
XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
PS Disclosure; Fig 30B; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antiangiogenic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents a human VEGF-X protein
CC described in the method of the invention.
XX
SQ Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 21; Length 345;
Best Local Similarity 99.4%; Pred. No. 7e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGORRGQTQAESNLSSKFFQSSNKEQNGVQDPQHERITVTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGQTQAESNLSSKFFQSSNKEQNGVQDPQHERITVTNGSIHS 60
```

Qy 61 PRFHTYPRNTVLVWRLVAVENWVQLTFDERFGLDEPDIDICKYDFVEVEEPESDGTIL 120  
 Db 61 PRFHTYPRNTVLVWRLVAVENWVQLTFDERFGLDEPDIDICKYDFVEVEEPESDGTIL 120  
 Qy 121 GRWCGSTVPGKQISKGNOIRIRFVSDYFSEPGFCIHYNVMPQFTEAVSPVLPSSA 180  
 Db 121 GRWCGSTVPGKQISKGNOIRIRFVSDYFSEPGFCIHYNVMPQFTEAVSPVLPSSA 180  
 Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLDELRYPTWQLLGKAFVFGKRSRVVDLNL 240  
 Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLDELRYPTWQLLGKAFVFGKRSRVVDLNL 240  
 Qy 241 LTEEVRVLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300  
 Db 241 LTEEVRVLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300  
 Qy 301 VTKYHEVLQRPKTGVRLHKSITDVALEHHEEDCVCRCSTGG 345  
 Db 301 VTKYHEVLQRPKTGVRLHKSITDVALEHHEEDCVCRCSTGG 345

## RESULT 12

AA10650  
 ID AAB10650 standard; Protein; 345 AA.

XX AAB10650;

XX DT 19-JAN-2001 (first entry)

XX DB Human 990126vegX protein.

XX KW VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;  
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;  
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
 KW venous sore; diabetic ulcer; burns; skin graft growth.

XX OS Homo sapiens.

XX PN WO200037641-A2.

XX PD 29-JUN-2000.

XX PF 21-DEC-1999; 99WO-US30503.

XX PR 22-DEC-1998; 98GB-0028377.

XX PR 18-MAR-1999; 99US-0124967.

XX PR 08-NOV-1999; 99US-0164131.

XX PA (JANC ) JANSEN PHARM NV.

XX PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;

XX PI Dhanaraj SN, Xu J;

XX DR WPI; 2000-442669/38.

XX PT New vascular endothelial growth factor protein, useful for treating or  
 PT preventing diseases associated with inappropriate angiogenesis activity  
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX PS Disclosure; Fig 11; 127pp; English.

XX CC This invention describes a novel vascular endothelial growth factor-X  
 CC (VEGF-X) protein (1a) and its encoding polynucleotide (1ia) which has  
 CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and  
 CC antidiabetic activity and acts as an angiogenesis and vascularization  
 CC regulator. An antisense molecule of the invention is useful for treating  
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
 CC retinopathy by inhibiting angiogenic activity or inappropriate  
 CC vascularization including formation and proliferation of new blood  
 CC vessels, growth and development of tissues, tissue regeneration and organ  
 CC and tissue repair in a subject. The products of the invention are useful

CC for preparing medicaments for treating wounds such as dermal ulcers,  
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
 CC skin graft growth, tissue repair, proliferation of new blood vessels,  
 CC tissue regeneration and organ repair by promoting angiogenic activity or  
 CC vascularization. This sequence represents the human 990126vegX protein  
 CC used to illustrate the method of the invention.

SQ Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 21; Length 345;  
 Best Local Similarity 99.4%; Pred. No. 7e-179; Indels 0; Gaps 0;  
 Matches 343; Conservative 2; Mismatches 0;

Qy 1 MSFLGLLLVTSALAGQRRGTAESNLSSKQFSSNKQGVQDPQHERIITVSTNGSIHS 60

Db 1 MSFLGLLLVTSALAGQRRGTAESNLSSKQFSSNKQGVQDPQHERIITVSTNGSIHS 60

Qy 61 PRFHTYPRNTVLVWRLVAVENWVQLTFDERFGLDEPDIDICKYDFVEVEEPESDGTIL 120

Db 61 PRFHTYPRNTVLVWRLVAVENWVQLTFDERFGLDEPDIDICKYDFVEVEEPESDGTIL 120

Qy 121 GRWCGSTVPGKQISKGNOIRIRFVSDYFSEPGFCIHYNVMPQFTEAVSPVLPSSA 180

Db 121 GRWCGSTVPGKQISKGNOIRIRFVSDYFSEPGFCIHYNVMPQFTEAVSPVLPSSA 180

Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLDELRYPTWQLLGKAFVFGKRSRVVDLNL 240

Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLDELRYPTWQLLGKAFVFGKRSRVVDLNL 240

Qy 241 LTEEVRVLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300

Db 241 LTEEVRVLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300

Qy 301 VTKYHEVLQRPKTGVRLHKSITDVALEHHEEDCVCRCSTGG 345

Db 301 VTKYHEVLQRPKTGVRLHKSITDVALEHHEEDCVCRCSTGG 345

## RESULT 13

AA10651  
 ID AAB10651 standard; Protein; 345 AA.

XX AC AAB10651;

XX DT 19-JAN-2001 (first entry)

XX DE Human VEGF-X protein #3.

XX KW VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;  
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;  
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
 KW venous sore; diabetic ulcer; burns; skin graft growth.

XX OS Homo sapiens.

XX PN WO200037641-A2.

XX PD 29-JUN-2000.

XX PF 21-DEC-1999; 99WO-US30503.

XX PR 22-DEC-1998; 98GB-0028377.

XX PR 18-MAR-1999; 99US-0124967.

XX PR 08-NOV-1999; 99US-0164131.

XX PA (JANC ) JANSEN PHARM NV.

XX PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;

XX PI Dhanaraj SN, Xu J;

XX DR WPI; 2000-442669/38.

XX New vascular endothelial growth factor protein, useful for treating or  
PT preventing diseases associated with inappropriate angiogenesis activity  
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -  
PS  
XX Claim 72; Fig 12; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X  
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has  
CC vulnerability, cytostatic, antirheumatic, antiarthritic, antipsoriatic and  
CC antidiabetic activity and acts as an angiogenesis and vascularization  
CC regulator. An antisense molecule of the invention is useful for treating  
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
CC retinopathy by inhibiting angiogenic activity or inappropriate  
CC vascularization including formation and proliferation of new blood  
CC vessels, growth and development of tissues, tissue regeneration and organ  
CC and tissue repair in a subject. The products of the invention are useful  
CC for preparing medicaments for treating wounds such as dermal ulcers,  
CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
CC skin graft growth, tissue repair, proliferation of new blood vessels,  
CC tissue regeneration and organ repair by promoting angiogenic activity or  
CC vascularization. This sequence represents the human VEGF-X protein  
CC described in the method of the invention.

XX Sequence 345 AA;  
SQ

Query Match 99.6%; Score 1851; DB 21; Length 345;  
Best Local Similarity 99.4%; Pred. No. 7e-179;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLLFGLLLVTSALAGQRQTQAEENLSKQFQSNKQNGVQDPQHERIITVSTNGSIHS 60  
DB 1 MSLLFGLLLVTSALAGQRQTQAEENLSKQFQSNKQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRPHTYPRNTLVWRLVAVENWVIOITDEREGLEDPEDDICKYDFVEEESDGTIL 120  
DB 61 PRPHTYPRNTLVWRLVAVENWVIOITDEREGLEDPEDDICKYDFVEEESDGTIL 120

QY 121 GRWCGSTVPFGKQISKGNQIRIRVSDYFPPSEFGFCHYHNVMPQTEAVSPVLPPSA 180  
DB 121 GRWCGSTVPFGKQISKGNQIRIRVSDYFPPSEFGFCHYHNVMPQTEAVSPVLPPSA 180

QY 181 LPDLNNATAFSTLEDLYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240  
DB 181 LPDLNNATAFSTLEDLYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240

QY 241 LTEEVRLYSCTPRNFSYVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300  
DB 241 LTEEVRLYSCTPRNFSYVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300

QY 301 VTKKYHEVLQRLPKTGVRLHKSITDVALEHHEECDCVCRGSTGG 345  
DB 301 VTKKYHEVLQRLPKTGVRLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 14  
AAB19578  
XX ID AAB19578 standard; Protein; 345 AA.  
XX AC AAB19578;  
XX DT 22-JAN-2001 (first entry)  
XX DE Human PRO200 (vascular endothelial growth factor E).  
XX KW PRO200; vascular epithelial growth factor E; VEGF-E; human;  
XX KW ocular disease; retinopathy; maculopathy; therapy;  
XX KW retinitis pigmentosa; macular degeneration; retinal detachment;  
XX KW retinal tear; macular hole; myopia; traumatic chorioretinopathy;  
XX KW acute retinal necrosis syndrome; contusion; edema;  
XX KW retinal vision occlusion; vascular disease; retinal vasculitis;  
XX KW thrombocytopenic purpura; uveitis; retinal occlusion.

OS Homo sapiens.  
XX Key Location/Qualifiers  
FT Peptide 1..14  
FT Protein /label= Signal\_peptide  
FT 15..345  
FT /label= Mature\_Pro200  
FT Modified-site 25..29  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 55..59  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 254..258  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 15..21  
FT /note= "N-myristoylation"  
FT Modified-site 117..123  
FT /note= "N-myristoylation"  
FT Modified-site 127..133  
FT /note= "N-myristoylation"  
FT Modified-site 281..287  
FT /note= "N-myristoylation"  
FT Modified-site 282..288  
FT /note= "N-myristoylation"  
FT Modified-site 319..325  
FT /note= "Amidation"

XX W0200053760-A2.  
XX 14-SEP-2000.  
XX 10-MAR-2000; 2000WO-US063119.  
XX 12-MAR-1999; 99US-0123957.  
XX (SETH ) GENENTECH INC.  
XX Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ, Kabakoff RC;  
XX Klein RD, Kijavini IJ, Kuo SS, La Fleur M, Wood WI;  
XX WPI; 2000-587437/55.  
XX N-PSDB; AAA88515.

XX Novel PRO polypeptides useful for preventing or rescuing retinal cells  
PT from injury caused by ocular diseases such as retinitis pigmentosa,  
PT retinopathy, retinal degenerative diseases, degenerative myopia,  
PT uveitis -  
XX Claim 2; Fig 2; 140pp; English.

The present sequence is that of human PRO200 or vascular endothelial growth factor E (VEGF-E), as predicted from a cDNA clone (see AAA88515) that was isolated from a glioma cell line G61. Library using probes (see AAA88523-26) based on an expressed sequence tag (see AAA88522) that showed homology to VEGF. PRO200 has a predicted mol.wt. of 39,029 and a pI of about 6.06. A method for producing PRO polypeptides, including PRO200, using a host cell transformed with a vector comprising a PRO nucleic acid is claimed. The invention relates to the use of PRO polypeptides to delay, prevent or rescue retinal cells such as retinal neurons selected from photoreceptors, retinal ganglion cells, displaced retinal ganglion cells, amacrine cells, displaced amacrine cells, horizontal and bipolar neurons, and supportive cells (including Mueller cells and pigment epithelial cells) from injury and degradation. The retinal cells are preferably photoreceptors and photoreceptor cell injury or death is caused by retinal injury, light or environmental trauma or by an ocular disease selected from retinitis pigmentosa, macular degeneration, including age-related, retinal detachment, retinal tears, retinopathy, retinal degenerative diseases, macular holes, degenerative myopia, acute retinal necrosis syndrome, traumatic chorioretinopathies or contusion such as Purtscher's retinopathy, edema, ischemic conditions such as central or branch retinal vision occlusion, collagen vascular diseases, thrombocytopenic purpura, uveitis, retinal vasculitis and occlusion associated with Bales

CC disease and systemic lupus erythematosus (claimed).

XX  
SQ Sequence 345 AA;  
Query Match 99.6%; Score 1851; DB 21; Length 345;  
Best Local Similarity 99.4%; Pred. No. 7e-179; Mismatches 0; Indels 0; Gaps 0;  
Matches 343; Conservative 2;  
QY 1 MSLFGLLLVTSALAGQRRGQAESNLSSKTFQSSNKQNGVQDPQHERIITVSTNGSIHS 60  
Db 1 MSLFGLLLVTSALAGQRRGQAESNLSSKTFQSSNKQNGVQDPQHERIITVSTNGSIHS 60  
QY 61 PRPHPTVPRNTLVWRVLAVERNWIQITDERFGLDEPDIDCKYDFVEEPEPSDGTIL 120  
Db 61 PRPHPTVPRNTLVWRVLAVERNWIQITDERFGLDEPDIDCKYDFVEEPEPSDGTIL 120  
QY 121 GRWCGSTVPGKQISKNQIRIRVSDYPPSEPGFCIHYNVMPQTEAVSPSVLPSSA 180  
Db 121 GRWCGSTVPGKQISKNQIRIRVSDYPPSEPGFCIHYNVMPQTEAVSPSVLPSSA 180  
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240  
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240  
QY 241 LTBVRLYSCTPNRFNSIREEELKRTDTIWPFGCLLVKRCGNCACCLHNCNECCVPSK 300  
Db 241 LTBVRLYSCTPNRFNSIREEELKRTDTIWPFGCLLVKRCGNCACCLHNCNECCVPSK 300  
QY 301 VTKYHEVLQRPKTGVRGLHKSITDVALBHEHRCDCVCRGSTGG 345  
Db 301 VTKYHEVLQRPKTGVRGLHKSITDVALBHEHRCDCVCRGSTGG 345

RESULT 15  
AAB33414  
ID AAB33414 standard; Protein; 345 AA.  
AC AAB33414;  
XX  
XX 29-JAN-2001 (first entry)  
XX Human PRO200 protein UNQ174 SEQ ID NO:2.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
KW haemostatic; antithyroid; antidiabetic; neutrotropic; neuroprotective;  
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW autoimmune disease; immune-mediated skin disease; allergic disease;  
KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease.

OS Homo sapiens.  
XX  
XX WC2000053758-A2.  
XX  
XX 14-SEP-2000.

XX 02-MAR-2000; 2000WO-US05841.  
XX  
XX 08-MAR-1999; 99WO-US05028.  
XX 10-MAR-1999; 99US-0123618.  
XX 12-MAR-1999; 99US-0123957.  
XX 23-MAR-1999; 99US-0125775.  
XX 12-APR-1999; 99US-0128849.  
XX 20-APR-1999; 99WO-US08615.  
XX 28-APR-1999; 99US-0131445.

PR 04-MAY-1999; 99US-0132371.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-OCT-1999; 99US-0162506.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30999.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 11-FEB-2000; 2000WO-US00376.  
PR 18-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.

(GETH ) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
PI Kabakoff RC, Lu Y, Fan J, Pennica D, Shelton DL, Smith V;  
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
XX WPI; 2000-572271/53.

DR N-PSDB; AAC58579.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
PS Claim 33; Fig 2; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can  
CC be used in the treatment of immune related diseases. The human PRO  
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
CC treating and diagnosing immune related disorders. The disorders are  
CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
CC autoimmune or immune-mediated skin diseases, allergic diseases,  
CC immunological diseases of the lung, and transplantation associated  
CC diseases including graft rejection and graft-versus-host-disease.  
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.

SQ Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 21; Length 345;  
Best Local Similarity 99.4%; Pred. No. 7e-179;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 21:04:39 ; Search time 24.3006 Seconds  
(without alignments)  
2618.575 Million cell updates/sec

Title: US-09-852-209A-3

Perfect score: 1858

Sequence: 1 MSFGLLLVTSALAGQRGT.....DVALEHHECDVCVRGSGTG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 18443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1858	100.0	345	9	US-09-818-943-1
2	1858	100.0	345	10	US-09-852-209A-3
3	1858	100.0	345	14	US-10-086-623-32
4	1858	100.0	345	15	US-10-260-539-32
5	1858	100.0	345	15	US-10-131-600-3
6	1851	99.6	345	9	US-09-823-033-2
7	1851	99.6	345	9	US-09-923-995-4
8	1851	99.6	345	10	US-09-795-006A-149
9	1851	99.6	345	10	US-09-978-295A-488
10	1851	99.6	345	10	US-09-978-597-488
11	1851	99.6	345	10	US-09-978-192A-488
12	1851	99.6	345	10	US-09-999-832A-488
13	1851	99.6	345	11	US-09-978-189-488
14	1851	99.6	345	11	US-09-796-753-6
15	1851	99.6	345	11	US-09-978-608A-488

16	1851	99.6	345	11	US-09-978-585A-488	Sequence 488, App
17	1851	99.6	345	11	US-09-978-191A-488	Sequence 488, App
18	1851	99.6	345	11	US-09-978-403A-488	Sequence 488, App
19	1851	99.6	345	11	US-09-978-564A-488	Sequence 488, App
20	1851	99.6	345	11	US-09-999-833A-488	Sequence 488, App
21	1851	99.6	345	11	US-09-981-915A-488	Sequence 488, App
22	1851	99.6	345	11	US-09-978-824-488	Sequence 488, App
23	1851	99.6	345	11	US-09-918-585A-488	Sequence 488, App
24	1851	99.6	345	11	US-09-978-423A-488	Sequence 488, App
25	1851	99.6	345	11	US-09-978-193A-488	Sequence 488, App
26	1851	99.6	345	11	US-09-999-830A-488	Sequence 488, App
27	1851	99.6	345	11	US-09-978-757A-488	Sequence 488, App
28	1851	99.6	345	11	US-09-978-187B-488	Sequence 488, App
29	1851	99.6	345	11	US-09-978-643A-488	Sequence 488, App
30	1851	99.6	345	12	US-09-978-375A-488	Sequence 488, App
31	1851	99.6	345	12	US-09-978-188A-488	Sequence 488, App
32	1851	99.6	345	12	US-09-978-298A-488	Sequence 488, App
33	1851	99.6	345	12	US-10-137-870-286	Sequence 286, App
34	1851	99.6	345	12	US-10-140-018-286	Sequence 286, App
35	1851	99.6	345	12	US-10-140-021-286	Sequence 286, App
36	1851	99.6	345	12	US-10-140-274-286	Sequence 286, App
37	1851	99.6	345	12	US-10-140-471-286	Sequence 286, App
38	1851	99.6	345	12	US-10-140-807-286	Sequence 286, App
39	1851	99.6	345	12	US-10-140-922-286	Sequence 286, App
40	1851	99.6	345	12	US-10-140-924-286	Sequence 286, App
41	1851	99.6	345	12	US-10-141-598-286	Sequence 286, App
42	1851	99.6	345	12	US-10-141-702-286	Sequence 286, App
43	1851	99.6	345	12	US-10-141-704-286	Sequence 286, App
44	1851	99.6	345	12	US-10-142-421-286	Sequence 286, App
45	1851	99.6	345	12	US-10-142-421-286	Sequence 286, App

ALIGNMENTS

RESULT 1

US-09-818-943-1  
; Sequence 1, Application US/09818943  
; Patent No. US20020049987A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: LI, Xuri  
; APPLICANT: FONTEN, Annica  
; APPLICANT: AASE, Karin  
; APPLICANT: LI, Hong  
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH  
; FILE REFERENCE: 1064/48487  
; CURRENT APPLICATION NUMBER: US/09/818,943  
; CURRENT FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/192,507  
; PRIOR FILING DATE: 2000-03-28  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-818-943-1

Query Match 100.0%; Score 1858; DB 9; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.1e-179;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVQDPQHERIIIVTNGSIHS 60

Db 1 MSFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVQDPQHERIIIVTNGSIHS 60

Qy 61 PRFPHYTPRNTLVWRLVAEENWVWLTQTFDEFGLEDPEDDICKYDFVEEPESDGTIL 120

Db 61 PRFPHYTPRNTLVWRLVAEENWVWLTQTFDEFGLEDPEDDICKYDFVEEPESDGTIL 120

Qy 121 GRWCGSTVPGKQISKGNQIRIRFVSDEYFPESEFGFCIHVNVMPQFTEAVSPVLPSPA 180



Db 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSEFGFCIHYNVMPQTEAVSPSLPPSA 180  
Qy 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240  
Db 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240  
Qy 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300  
Db 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300  
Qy 301 VTKYHEVLQRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345  
Db 301 VTKYHEVLQRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345

## RESULT 2

US-09-852-209a-3  
; Sequence 3, Application US/09852209A  
; Patent No. US20020164687A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETHSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/852,209A  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 3  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-852-209a-3

Query Match 100.0%; Score 1858; DB 10; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.1e-179;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
Db 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
Qy 61 PRPHTYPRNTVLVWRLVAEENVMQLTDFDRFGLDEPDDICKYDFVEVEEPPSDGTIL 120  
Db 61 PRPHTYPRNTVLVWRLVAEENVMQLTDFDRFGLDEPDDICKYDFVEVEEPPSDGTIL 120  
Qy 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSEFGFCIHYNVMPQTEAVSPSLPPSA 180  
Db 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSEFGFCIHYNVMPQTEAVSPSLPPSA 180  
Qy 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240  
Db 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240

Qy 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300  
Db 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300  
Qy 301 VTKYHEVLQRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345  
Db 301 VTKYHEVLQRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345

## RESULT 3

US-10-086-623-32  
; Sequence 32, Application US/10086623  
; Publication No. US20020164710A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LI, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES  
; FILE REFERENCE: 1064/44833C2  
; CURRENT APPLICATION NUMBER: US/10/086,623  
; CURRENT FILING DATE: 2000-03-04  
; PRIOR APPLICATION NUMBER: US 60/107,852  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: US 60/113,997  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: US 60/150,604  
; PRIOR FILING DATE: 1999-08-26  
; PRIOR APPLICATION NUMBER: US 60/157,108  
; PRIOR FILING DATE: 1999-10-04  
; PRIOR APPLICATION NUMBER: US 60/157,756  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: US 09/438,046  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 09/691,200  
; PRIOR FILING DATE: 2000-10-19  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 32  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Amino acid sequence for PDGF-C  
US-10-086-623-32

Query Match 100.0%; Score 1858; DB 14; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.1e-179;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
Db 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
Qy 61 PRPHTYPRNTVLVWRLVAEENVMQLTDFDRFGLDEPDDICKYDFVEVEEPPSDGTIL 120  
Db 61 PRPHTYPRNTVLVWRLVAEENVMQLTDFDRFGLDEPDDICKYDFVEVEEPPSDGTIL 120  
Qy 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSEFGFCIHYNVMPQTEAVSPSLPPSA 180  
Db 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSEFGFCIHYNVMPQTEAVSPSLPPSA 180  
Qy 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240  
Db 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240  
Qy 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300

Db 241 LTERVLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCQCVPK 300

Qy 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

Db 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 4

US-10-260-539-32

; Sequence 32, Application US/10260539

; Publication No. US20030073637A1

; GENERAL INFORMATION:

; APPLICANT: ERIKSSON, Ulf

; APPLICANT: AASE, Karin

; APPLICANT: LI, Xuri

; APPLICANT: PONTEN, Annica

; APPLICANT: UUTELA, Marko

; APPLICANT: ALITALO, Kari

; APPLICANT: OESTMAN, Arne

; APPLICANT: HELDIN, Carl-Henrik

; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THEREOF

; FILE REFERENCE: 1064/44833C2

; CURRENT APPLICATION NUMBER: US/10/260,539

; CURRENT FILING DATE: 2002-10-01

; PRIOR APPLICATION NUMBER: US/10/086,623

; PRIOR FILING DATE: 2000-03-04

; PRIOR APPLICATION NUMBER: US 60/107,852

; PRIOR FILING DATE: 1998-11-10

; PRIOR APPLICATION NUMBER: US 60/113,997

; PRIOR FILING DATE: 1998-12-28

; PRIOR APPLICATION NUMBER: US 60/150,604

; PRIOR FILING DATE: 1999-08-26

; PRIOR APPLICATION NUMBER: US 60/157,108

; PRIOR FILING DATE: 1999-10-04

; PRIOR APPLICATION NUMBER: US 60/157,756

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: US 09/438,046

; PRIOR FILING DATE: 1999-11-10

; PRIOR APPLICATION NUMBER: US 09/691,200

; PRIOR FILING DATE: 2000-10-19

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 32

; LENGTH: 345

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Amino acid sequence for PDGF-C

US-10-260-539-32

Query Match 100.0%; Score 1858; DB 15; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.1e-179;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLFGLLVTSALAQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60

Db 1 MSLFGLLVTSALAQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60

Qy 61 PRPPTYPRNTVLVWRLVAEENWVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120

Db 61 PRPPTYPRNTVLVWRLVAEENWVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120

Qy 121 GRWCSGTVPGKQISKGNQIRIRFVSDVEYFPSEPGFCIHYNVMPQFTEAVSPSVLPSPA 180

Db 121 GRWCSGTVPGKQISKGNQIRIRFVSDVEYFPSEPGFCIHYNVMPQFTEAVSPSVLPSPA 180

Qy 121 GRWCSGTVPGKQISKGNQIRIRFVSDVEYFPSEPGFCIHYNVMPQFTEAVSPSVLPSPA 180

Db 121 GRWCSGTVPGKQISKGNQIRIRFVSDVEYFPSEPGFCIHYNVMPQFTEAVSPSVLPSPA 180

Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLLGKAFVFGKRSRVVDLNL 240

Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLLGKAFVFGKRSRVVDLNL 240

Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLLGKAFVFGKRSRVVDLNL 240

Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLLGKAFVFGKRSRVVDLNL 240

Qy 241 LTERVLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCQCVPK 300

Db 241 LTERVLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCQCVPK 300

Db 241 LTERVLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCQCVPK 300

Qy 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

Db 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 5

US-10-131-600-3

; Sequence 3, Application US/10131600

; Publication No. US20030082670A1

; GENERAL INFORMATION:

; APPLICANT: ERIKSSON, Ulf

; APPLICANT: AASE, Karin

; APPLICANT: LEE, Xuri

; APPLICANT: PONTEN, Annica

; APPLICANT: UUTELA, Marko

; APPLICANT: ALITALO, Kari

; APPLICANT: OESTMAN, Arne

; APPLICANT: HELDIN, Carl-Henrik

; APPLICANT: BETSHOUTZ, Christer

; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING THEREFOR, AND USES THEREOF

; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740

; CURRENT APPLICATION NUMBER: US/10/131,600

; CURRENT FILING DATE: 2002-04-25

; PRIOR APPLICATION NUMBER: US/09/410,349

; PRIOR FILING DATE: 1999-09-30

; PRIOR APPLICATION NUMBER: 60/108,109

; PRIOR FILING DATE: 1998-11-12

; PRIOR APPLICATION NUMBER: 60/110,749

; PRIOR FILING DATE: 1998-12-03

; PRIOR APPLICATION NUMBER: 60/113,002

; PRIOR FILING DATE: 1998-12-18

; PRIOR APPLICATION NUMBER: 60/135,426

; PRIOR FILING DATE: 1999-05-21

; PRIOR APPLICATION NUMBER: 60/144,022

; PRIOR FILING DATE: 1999-07-15

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 3

; LENGTH: 345

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-131-600-3

Query Match 100.0%; Score 1858; DB 15; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.1e-179;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLFGLLVTSALAQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60

Db 1 MSLFGLLVTSALAQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60

Qy 61 PRPPTYPRNTVLVWRLVAEENWVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120

Db 61 PRPPTYPRNTVLVWRLVAEENWVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120

Qy 121 GRWCSGTVPGKQISKGNQIRIRFVSDVEYFPSEPGFCIHYNVMPQFTEAVSPSVLPSPA 180

Db 121 GRWCSGTVPGKQISKGNQIRIRFVSDVEYFPSEPGFCIHYNVMPQFTEAVSPSVLPSPA 180

Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLLGKAFVFGKRSRVVDLNL 240

Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLLGKAFVFGKRSRVVDLNL 240

Qy 241 LTERVLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCQCVPK 300

Db 241 LTERVLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCQCVPK 300

Qy 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

Db 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 6  
US-09-823-033-2

; Sequence 2, Application US/09823033  
; Patent No. US2002004225A1  
; GENERAL INFORMATION:  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Gilbertson, Debra G.  
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE  
; FILE REFERENCE: 00-12  
; CURRENT APPLICATION NUMBER: US/09/823,033  
; CURRENT FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-823-033-2

Query Match 99.6%; Score 1851; DB 9; Length 345;  
Best Local Similarity 99.4%; Pred. No. 1.6e-178;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSSNKQNGVQDPOHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSSNKQNGVQDPOHERIITVSTNGSIHS 60
Qy 61 PRFPHYTPRNTVLVWRLVAEENWVIQLTDFERFGLDEPDIDICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHYTPRNTVLVWRLVAEENWVIQLTDFERFGLDEPDIDICKYDFVEVEEPSDGTIL 120
Qy 121 GRWCGSGTVPGKQISKGNIQIRFVSDYFSEPGFCIHYNVMPQFTEAVSPSVLPSPA 180
Db 121 GRWCGSGTVPGKQISKGNIQIRFVSDYFSEPGFCIHYNVMPQFTEAVSPSVLPSPA 180
Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Qy 301 VTKEYHEVLQRLPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKEYHEVLQRLPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345
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RESULT 7  
US-09-923-995-4

; Sequence 4, Application US/09923995  
; Patent No. US20020081700A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNKI  
; FILE REFERENCE: 00-47  
; CURRENT APPLICATION NUMBER: US/09/923,995  
; CURRENT FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: US 60/223,164  
; PRIOR FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-923-995-4

Query Match 99.6%; Score 1851; DB 9; Length 345;  
Best Local Similarity 99.4%; Pred. No. 1.6e-178;

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Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSSNKQNGVQDPOHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSSNKQNGVQDPOHERIITVSTNGSIHS 60
Qy 61 PRFPHYTPRNTVLVWRLVAEENWVIQLTDFERFGLDEPDIDICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHYTPRNTVLVWRLVAEENWVIQLTDFERFGLDEPDIDICKYDFVEVEEPSDGTIL 120
Qy 121 GRWCGSGTVPGKQISKGNIQIRFVSDYFSEPGFCIHYNVMPQFTEAVSPSVLPSPA 180
Db 121 GRWCGSGTVPGKQISKGNIQIRFVSDYFSEPGFCIHYNVMPQFTEAVSPSVLPSPA 180
Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Qy 301 VTKEYHEVLQRLPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKEYHEVLQRLPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345
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## RESULT 8

US-09-795-006A-149  
; Sequence 149, Application US/09795006A  
; Patent No. US20020151680A1  
; GENERAL INFORMATION:  
; APPLICANT: Aitalo et al  
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
; FILE REFERENCE: 28967/35977B  
; CURRENT APPLICATION NUMBER: US/09/795,006A  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: US 60/205,331  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: US 60/185,205  
; PRIOR FILING DATE: 2000-02-25  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 149  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-795-006A-149

Query Match 99.6%; Score 1851; DB 10; Length 345;  
Best Local Similarity 99.4%; Pred. No. 1.6e-178;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSSNKQNGVQDPOHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSSNKQNGVQDPOHERIITVSTNGSIHS 60
Qy 61 PRFPHYTPRNTVLVWRLVAEENWVIQLTDFERFGLDEPDIDICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHYTPRNTVLVWRLVAEENWVIQLTDFERFGLDEPDIDICKYDFVEVEEPSDGTIL 120
Qy 121 GRWCGSGTVPGKQISKGNIQIRFVSDYFSEPGFCIHYNVMPQFTEAVSPSVLPSPA 180
Db 121 GRWCGSGTVPGKQISKGNIQIRFVSDYFSEPGFCIHYNVMPQFTEAVSPSVLPSPA 180
Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
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; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-30
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; PRIOR APPLICATION NUMBER: 60/084600
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match          99.6%; Score 1851; DB 10; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLVTSALAQQRGGTQAEGLSKQFSSNKEQNGVQDPQPHRIITVSTNGSIHS 60
DB 1 MSLFGLLVTSALAQQRGGTQAEGLSKQFSSNKEQNGVQDPQPHRIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLVRLVAEENWVQLTFDERFGLDEPDICKYDFVEVEPSDGTIL 120
;

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DB 61 PRFPHTYPRNTVLVRLVAEENWVQLTFDERFGLDEPDICKYDFVEVEPSDGTIL 120
QY 121 GRWCGSGTVPQKQISKGNQIRIRVSDYEYFSPSEPGFCIHNNVMPQTEAVSPVLPPSA 180
DB 121 GRWCGSGTVPQKQISKGNQIRIRVSDYEYFSPSEPGFCIHNNVMPQTEAVSPVLPPSA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLPERWQOLDLEDLYRPTWOLLGKAFVFGKRSRVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLPERWQOLDLEDLYRPTWOLLGKAFVFGKRSRVDLNL 240
QY 241 LTEEVRLYSCTPRNFSVIREELKRTDTIFMPGCLLVKRCGNCACCLHNCNECQVPSK 300
DB 241 LTEEVRLYSCTPRNFSVIREELKRTDTIFMPGCLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKYHEVLQLRPKTGVRLHKSITDVALEHHEBCDCVCRGSTGG 345
DB 301 VTKYHEVLQLRPKTGVRLHKSITDVALEHHEBCDCVCRGSTGG 345

RESULT 10
US-09-978-697-488
; Sequence 488, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC27
; CURRENT APPLICATION NUMBER: US/09/978,697
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649

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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match          99.6%; Score 1851; DB 10; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGLLVTSALAGORGTQAEENLSKQFQSNKQNGVQDPQDQHRITITVSTNGSIHS 60
Db 1 MSFLGLLVTSALAGORGTQAEENLSKQFQSNKQNGVQDPQDQHRITITVSTNGSIHS 60
QY 61 PRFHTYPRNVLVWRLVAVENWVQITQDERGLEDDPEDDICKYDFVEVEPSPDQITL 120
Db 61 PRFHTYPRNVLVWRLVAVENWVQITQDERGLEDDPEDDICKYDFVEVEPSPDQITL 120
QY 121 GRWCGSTVPKQISKGNIQIRFVSDRYFPSEFGFCHYINVMQPTAVSPSVLPSPA 180
Db 121 GRWCGSTVPKQISKGNIQIRFVSDRYFPSEFGFCHYINVMQPTAVSPSVLPSPA 180
QY 181 LPDLLNNAITAFSTLEDLIRVLEPERWQDLEDLIRPTWQLLCKAFVFGKRSVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRVLEPERWQDLEDLIRPTWQLLCKAFVFGKRSVVDLNL 240
QY 241 LTEEVRVLYSCPRNFSVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
Db 241 LTEEVRVLYSCPRNFSVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLQRPKTVGRLHLSLTDVALEHHERCDVCRCSTGG 345
Db 301 VTKKYHEVLQRPKTVGRLHLSLTDVALEHHERCDVCRCSTGG 345

RESULT 11
US-09-978-192A-488
; Sequence 488, Application US/09978192A
; Patent No. US2002017553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumaas, Daniel
; APPLICANT: Williams, P. Wickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC9
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
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; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
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; PRIOR APPLICATION NUMBER: 60/080334
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; PRIOR FILING DATE: 1998-04-08
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; PRIOR FILING DATE: 1998-04-08
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; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
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; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
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; PRIOR FILING DATE: 1998-04-15
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; PRIOR FILING DATE: 1998-04-22
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; PRIOR FILING DATE: 1998-04-22
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; PRIOR APPLICATION NUMBER: 60/084643
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; PRIOR APPLICATION NUMBER: 60/085339
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; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13

; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 10; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFGLLLVTSALAGORGTQAESNLSSKFPQSSNKEQNGVDPQHERIITVSTNGSIHS 60
Db 1 MSFGLLLVTSALAGORGTQAESNLSSKFPQSSNKEQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLVWRLVAEENVWLTQTFDERFGLDEPDDICKYDFVEVEPSDGTIL 120
Db 61 PRFPHTYPRNTVLVWRLVAEENVWLTQTFDERFGLDEPDDICKYDFVEVEPSDGTIL 120
QY 121 GRWCGSGTVGKQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPOFTAVSPSVLPSSA 180
Db 121 GRWCGSGTVGKQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPOFTAVSPSVLPSSA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWOLDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWOLDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240
QY 241 LTBVRLYSCTPRNFSVIREELKRTDTTPWPGCLLVKRCGGNACCLHNCNCCQVPSK 300
Db 241 LTBVRLYSCTPRNFSVIREELKRTDTTPWPGCLLVKRCGGNACCLHNCNCCQVPSK 300
QY 301 VTKKHEVLQLRPKTVGRGLHKSITDVALHHEECDCVCRGSGTGG 345
Db 301 VTKKHEVLQLRPKTVGRGLHKSITDVALHHEECDCVCRGSGTGG 345

RESULT 12
US-09-999-832A-488
; Sequence 488, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
```

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
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PRIOR APPLICATION NUMBER: 60/084598

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; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 10; Length 345;

Best Local Similarity 99.4%; Pred. No. 1.6e-178;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGLLVTALACORGTQAESNLSSKFOFSSNKQGVQDPQHERIIIVTNGSIHS 60  
DB 1 MSFLGLLVTALACORGTQAESNLSSKFOFSSNKQGVQDPQHERIIIVTNGSIHS 60  
QY 61 PRPFHTYPRNTLVWRLVAEENWVIQLTDFRFGLEDPEDDICKYDFVEVEEFSDDGTL 120  
DB 61 PRPFHTYPRNTLVWRLVAEENWVIQLTDFRFGLEDPEDDICKYDFVEVEEFSDDGTL 120  
QY 121 GRWCGSTVPKGQISKGNIQIRFVSDYFEPSEPGFCIHYINVMPQFTEAVSPVLPPSA 180  
DB 121 GRWCGSTVPKGQISKGNIQIRFVSDYFEPSEPGFCIHYINVMPQFTEAVSPVLPPSA 180  
QY 181 LPDLILNNAITAFSTLEDLIRVLEPERWQDLEDLYRPTWOLLGKAFVFGKSRVVDLNL 240  
DB 181 LPDLILNNAITAFSTLEDLIRVLEPERWQDLEDLYRPTWOLLGKAFVFGKSRVVDLNL 240  
QY 241 LTERVRLYSCTPRNFVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300  
DB 241 LTERVRLYSCTPRNFVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300  
QY 301 VTKKYHEVLQRPKTVGRGLHKLSTDVALLHHEECDCVCRGSTGG 345  
DB 301 VTKKYHEVLQRPKTVGRGLHKLSTDVALLHHEECDCVCRGSTGG 345

RESULT 13

US-09-978-189-488  
; Sequence 488, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC7  
; CURRENT APPLICATION NUMBER: US/09/978,189  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 11; Length 345;  
Best Local Similarity 99.4%; Pred. No. 1.6e-178;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSLFGLLLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS	60
Db	1	MSLFGLLLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS	60
Qy	61	PRPPTYPRNTVLVWRLVAVEENVWVQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL	120
Db	61	PRPPTYPRNTVLVWRLVAVEENVWVQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL	120
Qy	121	GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPSPGFCIHYNIVMPQTEAVSPSVLPSSA	180
Db	121	GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPSPGFCIHYNIVMPQTEAVSPSVLPSSA	180
Qy	181	LPLDLNNAITAFSTLLEDLIRYLEPERWQLDLEDLIRPTWQLLGKAFVFGKRSRVVDNL	240
Db	181	LPLDLNNAITAFSTLLEDLIRYLEPERWQLDLEDLIRPTWQLLGKAFVFGKRSRVVDNL	240
Qy	241	LTEEVRLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQVPSK	300
Db	241	LTEEVRLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQVPSK	300
Qy	301	VTKKYHEVLQLRPKTGVRGLHKSLLTDVALEHHEECDCVCRGSGTGG	345
Db	301	VTKKYHEVLQLRPKTGVRGLHKSLLTDVALEHHEECDCVCRGSGTGG	345

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; Sequence 6, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
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; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
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; PRIOR FILING DATE: 1999-07-30
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; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
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; PRIOR FILING DATE: 1999-12-29
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; PRIOR FILING DATE: 2000-05-14
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; PRIOR APPLICATION NUMBER: 09/606,565
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; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 6
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-796-753-6

Query Match          99.6%; Score 1851; DB 11; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MSIFGLLIVTSALAGQRGCTQAESNLSSKFQFSSNKEQNGVDPQHRIITVTSTNGSIHS 60
; Sequence 6, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
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; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 6
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-796-753-6

Query Match          99.6%; Score 1851; DB 11; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MSIFGLLIVTSALAGQRGCTQAESNLSSKFQFSSNKEQNGVDPQHRIITVTSTNGSIHS 60

```

```
Db      1  MSIFGLLLTSALAGQGTQAESNLSSKFQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Qy      61  PRFHTYPRNTVLWRLVAVENWVIQLTFDEREGLEDPEDDICKYDFVEVEEPPSDGTIL 120
Db      61  PRFHTYPRNTVLWRLVAVENWVIQLTFDEREGLEDPEDDICKYDFVEVEEPPSDGTIL 120
Qy     121  GRWCGSTVPGKQISKGNQIRIRFVSDEYFPSEFGFCIHYNIVMPQFTEAVSPSVLPSSA 180
Db     121  GRWCGSTVPGKQISKGNQIRIRFVSDEYFPSEFGFCIHYNIVMPQFTEAVSPSVLPSSA 180
Qy     181  LPLDLLNNAITAPSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDNL 240
Db     181  LPLDLLNNAITAPSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDNL 240
Qy     241  LTEVRLYSCTPRNFSYSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db     241  LTEVRLYSCTPRNFSYSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Qy     301  VTKKYHEVLQIRPKTGVRLHKSITDVALEHHECDVCVRGSTGG 345
Db     301  VTKKYHEVLQIRPKTGVRLHKSITDVALEHHECDVCVRGSTGG 345
```

Search completed: November 25, 2003, 21:17:04  
Job time : 25.3006 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:59:34 ; Search time 14.7173 Seconds  
(without alignments)  
2254.373 Million cell updates/sec

Title: US-09-852-209A-3  
Perfect score: 1858  
Sequence: 1 MSLFGLLVTSALAGQRRGT.....DVALEHHEEDCVCRGSGTGG 345

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	742.5	40.0	370	JC7591	spinal cord-derive
2	736	39.6	370	JC7592	spinal cord-derive
3	183	9.8	3623	T09456	intrinsic factor-B
4	181.5	9.8	730	BMH1	procollagen C-endo
5	179.5	9.7	927	JQ0948	A5 antigen precurs
6	176	9.5	707	JC2218	procollagen C-endo
7	176	9.5	3623	T08618	intrinsic factor-B
8	173	9.3	823	A58788	procollagen C-endo
9	169	9.1	986	B58788	procollagen C-endo
10	169	9.1	991	I49540	procollagen C-endo
11	154	8.3	449	A55362	procollagen I C-pr
12	148.5	8.0	1057	A39288	dorsal-ventral pat
13	143.5	7.7	686	A59271	Ra-reactive factor
14	139.5	7.5	1070	T31069	tolloid-BMP-I like
15	138.5	7.5	597	S71352	metalloproteinase
16	138	7.4	705	CIHURB	complement subcomp
17	137.5	7.4	699	I54763	Ra-reactive factor
18	137.5	7.4	1524	T30337	polyprotein - Afri
19	133	7.2	1594	T30549	hensin - rabbit
20	132	7.1	419	S69207	vascular endotheli
21	130.5	7.0	1464	S58984	development protei
22	128	6.9	402	JH0403	procollagen I C-pr
23	127.5	6.9	767	T30018	hypothetical prote
24	127.5	6.9	3871	T22812	hypothetical prote
25	125	6.7	198	J50735	platelet-derived g
26	123.5	6.6	277	A41735	hyaluronate-bindin
27	123.5	6.6	579	JC7629	membrane-type friz
28	120.5	6.5	245	1 TVCITS	platelet-derived g
29	120.5	6.5	275	JC6506	tumor necrosis fac

ALIGNMENTS

RESULT 1

JC7591  
spinal cord-derived growth factor-B precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 24-Aug-2001  
C:Accession: JC7591  
R:Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.  
Biochem. Biophys. Res. Commun. 280, 733-737, 2001  
A:Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-  
A:Reference number: JC7591; MUID:21092670; PMID:11162582  
A:Accession: JC7591  
A:Molecule type: DNA  
A:Residues: 1-370 <HAM>  
A:Cross-references: DDBJ:AB033832  
C:Genetics:  
A:Gene: scdgf-B  
F:1-17/Domain: secretory signal sequence #status predicted <SIG>  
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAG>  
F:52-170/Region: CUB domain #status predicted  
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial gr  
F:294-308/Region: conserved motif #status predicted

Query Match 40.0%; Score 742.5; DB 2; Length 370;

Best Local Similarity 43.6%; Pred. No. 9e-57;  
Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;

QY 3 LFGLLVTSALAGQRRGTQAESNLSSKFPQSSN---KEQNGVOD-POHERIITVSTNGSI 58

DB 5 IFVYTLICANFSCSDTSAEQSASIKALRNANLRRDESNNHLLDLYRRDETIOVKGNGYV 64

QY 59 HSPRPHTYPRNTVLVWRLVAEENWVQLTFDRFGLEDPEDDCKYDFVEVEPSDGT 118

DB 65 QSPRPFSYPRNLLLTWRHLS-QENTRIQLVDFNQFGLAEANDICRYDFVEVEDSETS 123

QY 119 --ILGRVCGSTVPGKQISGNQIRIFVSDVFPSPGFCIHYNIVMPOFTAV----- 171

DB 124 TIIRKRWGCHKEVPPRIKSRNQLKITFKSDDTFVAPRGKIYSL-LEDPQPAASETN 182

QY 172 -----SPSLPPSALPLDLNNAITAFSTLEDLIRYLEPERWQDLEDLYR 217

DB 183 WESVTSISGVSNSPSVTDPT-LIADALOKIAEPDVEDLLKYFPESWQEDLENMVL 241

QY 218 PTWQLLKAFVFGKSRVDNLNLTTEVRLVYSCSTPRNFSVIREELKRTDTIEMPGCLV 277

DB 242 DTPRYGRSY-HSRKSK-VLDRLNDADKRYSTPRNYSVNIIEELKLANVFFPRCLLV 299

QY 278 KRCCGNCACCIHNCNECCQVPSKVTKYHEVQLRPP---KTGVRGLHKSITDVALEHHEE 334

DB 300 QRCGNGCGGTWNRSCTNSGKTVKTYHEVQLQEPGHKRRGRKAKTMALVDIQLDHER 359

QY 335 CDCVC 339

|||||



Db 360 CDCIC 364

RESULT 2

JC7592

C:Superfamily: intrinsic factor-B precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 24-Aug-2001

C:Accession: JC7592

R:Hamada, T.; Ui-Tai, K.; Imaki, J.; Miyata, Y.

Biochem. Biophys. Res. Commun. 280, 733-737, 2001

A:Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDFG/PDGF-C/spinal cord-derived growth factor-B precursor - rat

A:Reference number: JC7591; MUID:21092670; PMID:11162582

A:Contents: Fetal brain

A:Accession: JC7592

A:Molecule type: mRNA

A:Residues: 1-370 <HAM>

A:Cross-References: DDBJ:AB052170

C:Genetics:

A:Gene: scdf-B

P:1-17/Domain: secretory signal sequence #status predicted <SIG>

P:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>

F:52-170/Region: CUB domain #status predicted

F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial growth factor

F:294-308/Region: conserved motif #status predicted

Query Match 39.6%; Score 736; DB 2; Length 370;

Best Local Similarity 45.6%; Pred. No. 3.3e-56;

Matches 149; Conservative 57; Mismatches 93; Indels 28; Gaps 9;

QY 37 EQNGVQD-POHERIIIVTNGSIHSPRPHPTVPRNTVLVRLVAVENWIOITFDERG 95

Db 42 ESNHLTDLVRRDENIRVTGTHVQSPFPNSVPRNLLTLWRLHS-QEKTRIQALAFDHPG 100

QY 96 LEDPEDDICKYDFVEVEESDGT--ILGWGSGITVPGQISKGNOIRIRFVDSVFPSE 153

Db 101 LEEANDICRYDFVEVEDVESSTVVRGWCQGHKEIPRITRTNQIKITFQSDDYFVAK 160

QY 154 PGFCIHYNIV--MPQFTEAV-----SPSLPPSALPLDNLNNAITAFST 195

Db 161 PGFKIYYSFVEDFQFEAAEINWESVTSFSGVSHSPSVW-DSTLTADALOKIAEFT 219

QY 196 LEDLRYLEPERWQDLEDLYPTWQLLQKAFVFGKSRVVDNLNLTTEVRLYSCTPRNF 255

Db 220 VEDLLKYFNPAWQDLENLYMDTPRYGRSY-HERKSK-VDLDRINDVDKRYSCTPRNH 277

QY 256 SVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPSKVTKYHVLQIRP-- 313

Db 278 SVNREELKLTNAVFPFRCLLVQRCGNCGCGTLNWKSCVCSGKTVKKYHVLKRFEPGH 337

QY 314 -KTGVRGLHKSITDVALEHHEECDCVC 339

Db 338 FRRGKAKNMAVLDIQLDHERCDCIC 364

RESULT 3

T09456

C:Superfamily: intrinsic factor-B precursor - human

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 02-Aug-2002

C:Accession: T09456

R:Kozuyaki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Tommerup, N.

Blood 91, 3593-3600, 1998

A:Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characterization.

A:Reference number: Z16677; MUID:98241400; PMID:9572993

A:Accession: T09456

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-3623 <KOZ>

A:Cross-References: EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g3929529

C:Genetics:

A:Map position: 10p12

C:Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology

C:Keywords: receptor; vitamin B12 uptake

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>

F:436-467/Domain: EGF homology <EGF>

Query Match 9.8%; Score 183; DB 2; Length 3623;

Best Local Similarity 26.2%; Pred. No. 8.2e-07;

Matches 96; Conservative 42; Mismatches 139; Indels 90; Gaps 23;

QY 19 GTQAESNLSSKQF-----SSNEQNG-----VQDPQHERIIIVTNGSIHSPRPH 65

Db 892 GTDIPSFITSVYNELVYTVFKSSSTENHGFMKFAEDLACGELLTEST-GTIQSPGHPN 950

QY 66 TYPRNTVLVRLVAVENWIOITFDERGLDDEDDICKYDFVVEEESDGTILGRWCG 125

Db 951 VYPHGINCTWHIL-VQPNHLIHLMP-ETPHLEFHYN--CTNDYLEVYDTSLSGRYCG 1006

QY 126 SGTVPKGQISKGNOIRIRFVSDYFSPSPGFCIHYNIV-----MPQFTEAVSPSLPPS 179

Db 1007 K-SIPPSLTSSGNSLMVFTVDSDLAYE-GFLINVEAISAACTACQDYDDLTFTSP-- 1062

QY 180 ALPDLNNAITAFSTLEDLIRYLPFRWQDLEDLYR---PTWQLLQKAFVFGKSRVV 236

Db 1063 ----NFPNN-----YNNW---ECIYRITVTRTQQLIAVHFTNFSLEAI 1099

QY 237 DINLITE--EVR-----LY--SCTPRNVSISREELK-RTDPI-----FW 271

Db 1100 G-NYITDFLEIRDGGVYKSPLLGIFYGSLNLPPTIISHSNKMLKPKSDQIDTRSGFSAYW 1158

QY 272 PGCLLVKRCGNCACCLHNCNCCQVPSKVTKYHE--VLQLRPKTVGRGLHKSITDVA 328

Db 1159 DGS--STGCCGN-----LITSSGTFISPNYPMYHSHSECYWLLKSSHG-SAFELEPKDFH 1211

QY 329 LEHHEEC 335

Db 1212 LEHHPNC 1218

RESULT 4

BMHUI

procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human

N:Alternate names: bone morphogenic protein 1 (BMP1)

C:Species: Homo sapiens (man)

C:Date: 16-Sep-1992 #sequence\_revision 03-Aug-1995 #text\_change 18-Jun-1999

C:Accession: A37278; E58788

R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; H.

Science 242, 1528-1534, 1988

A:Title: Novel regulators of bone formation: molecular clones and activities.

A:Reference number: A37278; MUID:89072730; PMID:3201241

A:Accession: A37278

A:Molecule type: mRNA

A:Residues: 1-730 <WOZ>

A:Cross-References: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500

C:Genetics:

A:Gene: GDB:BMP1

A:Cross-References: GDB:125203; OMIM:112264

A:Map position: 8p21-8p21

C:Function:

A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen ty

C:Superfamily: procollagen C-endopeptidase; aspartic homology; C1r/C1s repeat homology;

C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication;

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>

F:130-321/Domain: aspartic homology <AST>

F:322-431/Domain: C1r/C1s repeat homology <CIR1>

F:435-544/Domain: C1r/C1s repeat homology <CIR2>

F:551-587/Domain: EGF homology <EGF>

F:591-700/Domain: C1r/C1s repeat homology <CIR3>

F:911-142,332,343,599/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-

F:213,217,223/Binding site: zinc (His, His, His, Tyr) #status predicted

F:214/Active site: Glu #status predicted

Gene 134, 257-261, 1993  
A>Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic pro  
A;Reference number: JC2218; MUID:94085787; PMID:8262384  
A;Accession: JC2218  
A:Molecule type: mRNA  
A;Residues: 1-707 <NAE>  
A;Cross-references: GB:L12249; NID:g406540; PIDN:AAA16313.1.; PID:g406541  
C;Comment: This protein induces ectopic cartilage formation in vivo.  
C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology;  
C;Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc  
F;93-284/Domain: astacin homology <AST>  
F;285-397/Region: complement 1r/1s-like repeat  
F;298-394/Domain: C1r/C1s repeat homology <ClR1>  
F;398-510/Region: complement 1r/1s-like repeat  
F;398-507/Domain: C1r/C1s repeat homology <ClR2>  
F;514-550/Domain: EGF homology <EGF>  
F;554-666/Region: complement 1r/1s-like repeat  
F;554-663/Domain: C1r/C1s repeat homology <ClR3>  
F;62,105,295,326/Binding site: carbohydrtate (Asn) (covalent) #status predicted  
F;176,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted  
F;177/Active site: Glu #status predicted  
F;528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match            9.5%; Score 176; DB 2; Length 707;  
Best Local Similarity 43.3%; Pred.No.4.2e-07;  
Matches 45; Conservative 15; Mismatches 36; Indels 8; Gaps 5;

Qy         55 NGSTHSFRPHYTPRNVLVRLVAENVVIQLTFDERGLEDDPEDDICKYDFVEVEE- 113  
            |||||:::||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db         562 NGSINSFGWPEYPPNNCNIMQLVAPQ-YRISLKFDQ---FETGNDVCCKDYDFVEVRSG 617  
            |||||:::||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy         114 -PSDGTILRCGSGTVPKGKIQISKGNQIRIRFSVDYEPSPPGF 156  
            |||||:::||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db         618 LTSDSKLGRKFCGS-ELPAVITSYNNWRIFPKSDNTV-SKKGF 659  
            |||||:::||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 7  
T08618  
Intrinsic factor-B12 receptor CUBILIN precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 02-Aug-2002  
C;Accession: T08618  
R;Moestrup, S.K.; Kosyraki, R.; Kristiansen, M.; Kayesen, J.H.; Rasmussen, H.H.; Brault  
J. Biol. Chem. 273, 5235-5242, 1998  
A>Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies  
A;Reference number: Z16459; MUID:98148073; PMID:9478979  
A;Accession: T08618  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A;Residues: 1-3623 <MOE>  
A;Cross-references: EMBL:AF022247; NID:g3834379; PIDN:AAC71661.1.; PID:g3834380  
C;Genetics:  
A;Gene: CUBILIN  
C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology  
C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>  
F;133-164/Domain: EGF homology <EGF1>  
F;436-467/Domain: EGF homology <EGF>

Query Match            9.5%; Score 176; DB 2; Length 3623;  
Best Local Similarity 25.5%; Pred.No.3.3e-06;  
Matches 95; Conservative 52; Mismatches 133; Indels 92; Gaps 24;

Qy         2 SLFGLLVLT--SALAGRRGTQAESNLSSKFQPSNKQNGVQDPQHERIIVTSNGSIH 59  
            ::||::||::||::||::||::||::||::||::||::||::||::||  
Db         901 SVVNILAVTVFKSSSMENRGFTA-----KFSDKLCEG-----EVLTAST-GITE 944  
            ::||::||::||::||::||::||::||::||::||::||::||::||

Qy         60 SPREFHYTPRNVLVRLVAENVVIQLTFDERGLEDDPEDDICKYDFVEVEESDGTT 119  
            ::||::||::||::||::||::||::||::||::||::||::||::||

Db         945 SPGHNVYPGVNCVTWHVV-VQRGLRIKRFPSS-FYLEPHEYN--CTNDYLELYDTAAQTFF 1000  
            ::||::||::||::||::||::||::||::||::||::||::||::||

Qy         120 LGRWCWGSGTVPKGKIQISKGNQIRIRFSVDYEPSPFGCIHV-----NIVMPQFTFAVSF 173  
            ::||::||::||::||::||::||::||::||::||::||::||::||



A/Accession: A59271  
 A/Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-696 <GEN>  
 A/Cross-references: GB:Y09926; NID:g4007626; PIDN:CAA71059.1; PID:g4007627  
 A/Experimental source: tissue liver  
 A/Note: submitted to Genbank, December 1996  
 A/Note: parts of this sequence, including the amino end of the mature protein, were deleted  
 C/Genetics:  
 A/Gene: GDB:MASP2  
 A/Cross-references: GDB:6071500

```

A:Map position: lp36.2-2-lp36.3
C:Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H
C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine p
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F:19-134/Domain: C1r/C1s repeat homology <C1R1>
F:142-180/Domain: EGF homology <EGF>
F:184-293/Domain: C1r/C1s repeat homology <C1R2>
F:300-361/Domain: complement factor H repeat homology <FHL>
F:366-430/Domain: complement factor H repeat homology <FHD>
F:445-679/Domain: trypsin homology <TRY>
F:72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,
F:158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:444-445/Cleavage site: Arg-Ile (autolytic) #status predicted
F:483,532,633/Active site: His, Asp, Ser #status predicted

Query Match          7.7%   Score 143.5;   DB 1;   Length 686;
Best Local Similarity 32.1%;   Pred. No. 0.00027;
Matches 34;   Conservative 25;   Mismatches 42;   Indels 5;   Gaps 4;

QY  55  NGSIHSRPFHTYPRNTVLVRLVAENVYVIQITDFERFGLGDPEDDICKYDFVEVEEP 114
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   193  SGELSSFEYPRPYKLSSTCYIS-LSLEGFSVILDFVESDFVETHPTLCYDFLKIQ-- 249

QY  115  SDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDSEYFPSPGFCIH 160
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   250  TDREEHGFPGCK-TLPHRIETKGNVTITVFVTOE-SGDHTGWKIH 293

```

RESULT 14

T31069

tolloid-BMP-1 like protein 1 - California sea hare  
N;Alternate names: Probable metalloprotease TBL-1  
C;Species: *Aplysia californica* (California sea hare)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 18-Aug-2000  
C;Accession: T31069  
R;Ilu, Q.R.; Hataar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Cleary, L.J.; Byrne, J.H.; Es  
J. Neurosci. 17, 753-764, 1997  
A;Title: A developmental gene (Tolloid/BMP-1) is regulated in *Aplysia* Neurons by treatme  
A;Reference number: Z20365; MUID:98007484; PMID:8987797  
A;Accession: T31069  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: mRNA  
A;Residues: 1-1070 -LIU->  
A;cross-references: EMBL:U57369; NID:g1899041; PID:g1899042; PIDN:AAC47485.1  
C;Superfamily: Dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s respo

Query Match	7.5%;	Score 139.5;	DB 2;	Length 1070;
Best Local Similarity	21.9%;	Pred. No. 0.0011;		
Matches	70;	Conservative	36;	Mismatches 102; Indels 111; Gaps 17;
QY	56	GSIHSPRFPHYPRNTVLVRLVAEENVVIQL---	TFDERFGLDEDDICKYDFVEVE	112
Db	529	GLNSPAIPDEYSGDKCEW-VIIVREGYQVALEFATFETF---	D8D---CAYDYVEIR	581
QY	113	--EPSPDITLGRWCWGSGTVPGKQLSKNQIRIRFVSDEYFPSEPGFCIHV-----	160	
Db	582	DGDTKPSLVGTTCGTFT-PPNALTSRHLVYKPVSDSM-QKGGFSAVLEEDVECEGE	639	
QY	161	-----	NTVMQPFTEAVSPSV	175
Db	640	DHGCEHVCVNTLGSYECTCKIGVELHSDGKKCEKACGGYLDAPSGTISSPF-----	PDL	694
QY	176	LPESAFLDLLNNAITAFS-----	TLEDLTRYLEPERWQLDLEDLYRPTWQLTGKARVFG	230
Db	695	YPPD-----KNCVWHISAPKGHTLVNFTMDLE-WRGDECEL-----	DFVRVTNVWG	741
QY	231	RKSRVVDLNLITBEVRLYSCTPRNFVS--IRBELKRTDITFWPGCLL-----	VKRCGGN	283
Db	742	NKER-----	LOGQYCGFMAPPISITLSNELRIEFRSDDTLQKTGFSMDYVADVDECASS	795
QY	284	CACLLHNCN-----	ECQC	296

796 NGGCKHICENTVGSFHCSC 814

RESULT 15

S71352

metalloproteinase (EC 3.4.24.-) 10 precursor, blastula - sea urchin (Paracentrotus lividus)

N:Alternate names: gene tolloid protein homolog

C:Species: Paracentrotus lividus (common urchin)

C:Date: 12-Feb-1998 #sequence revision 13-Mar-1998 #text\_change 17-Mar-1999

C:Accession: S71352; A44880; S22060

R:Homond, G.; Ghiglione, C.; Lepage, T.; Gache, C.

Eur. J. Biochem. 238, 744-751, 1996

A:Title: Structure of the gene encoding the sea urchin blastula protease 10 (BP10), a

A:Reference number: S71352; MUID:96300240; PMID:8706676

A:Accession: S71352

A:Molecule type: DNA

A:Residues: 1-597 <LHO>

A:Cross-references: EMBL:X65721; NID:e956534; PID:e46942

A:Experimental source: sperm

A:Note: the authors translated the codon GCT for residue 11 as Val, AAC for residue 57

R:Lepage, T.; Ghiglione, C.; Gache, C.

Development 114, 147-163, 1992

A:Title: Spatial and temporal expression pattern during sea urchin embryogenesis of a

ral patterning gene tolloid.

A:Reference number: A44880; MUID:92249197; PMID:1339338

A:Accession: A44880

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-7,'S',9-10,'V',12-28,'H',30-72,'D',74-77,'SK',80-81,'I',83-232,'R',234-2

9-57L,'N',573-584,'D',586-595,'D',597 <LSP>

A:Cross-references: EMBL:X56224; NID:g10928; PID:g10929

A:Experimental source: embryo

A:Note: sequence extracted from NCBI backbone (NCBIP:99979)

C:Genetics:

A:Gene: BP10

A:Introns: 30/3; 116/1; 184/3; 252/3; 370/3; 555/2

C:Superfamily: C1r/C1s repeat homology; astacin homology

C:Keywords: hydrolase; metalloproteinase; zinc

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-597/Product: metalloproteinase 10, blastula #status predicted <MAT>

F:102-295/Domain: astacin homology <AST>

F:339-446/Domain: C1r/C1s repeat homology <C1R1>

F:484-592/Domain: C1r/C1s repeat homology <C1R2>

F:130,194,200/Binding site: zinc (His) #status predicted

F:191/Active site: Glu #status predicted

Query Match 7.5%; Score 138.5; DB 2; Length 597;

Best Local Similarity 24.4%; Pred. No. 0.00062;

Matches 59; Conservative 44; Mismatches 92; Indels 47; Gaps 13;

QY 56 GSIIHSPRPHTYPRNTVLVRLVAVERNVMQLTFDERFGLDEDDICKYDFVEVEEP- 114

Db 348 GVITSPNPGRYDDNMACVQIEGPGGST-IELFTT- ---MNIENHAVCRYDAVEIRKDD 403

QY 115 --SDGTILGWCSGSTGVFGKQISKGNIQIRFVSDYFPSPGFCIHVNIWMPQFTEAVS 172

Db 404 INSDGE---KFCGN-TLPAQVQISSGNQMLYSFTSDPSITGR-GFRATYRIVILTTQPLD 458

QY 173 PSLVPSALPLDLLNNAIT-----AFSTLEDLI---RYLEPERWQDLEDLYRPT 219

Db 459 TTTTI-STTTTPVTTTQATTDVTVGSCGRFGGTQGRVATPNY--PNNYDNDLECVVIE 515

QY 220 WOLLGKAFVGRKSRVVDNLLTEEVRLYSCYTPNFSVSIREELKRTDITFWPCLLVKR 279

Db 516 VEV-----GRRVELDFIDVLEDET--NCRWDSUSINLGDGIK-----IDMKM 556

QY 280 CG 281

Db 557 CG 558

Search completed: November 25, 2003, 21:05:29

Job time : 15,7173 secs

Search completed: November 25, 2003, 21:05:29  
Job time : 15.7173 secs

---

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:55:48 ; Search time 8.55655 Seconds  
(without alignments)  
1896.117 Million cell updates/sec

Title: US-09-852-209A-3

Sequence: 1 MSUFGLLVTSALAQRRGT.....DVALEHHECDVCVRGSGTGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179.5	9.7	928	1 NRPI_XENLA	P28824 xenopus lae
2	176	9.5	707	1 NRPI_XENLA	P98070 xenopus lae
3	173.5	9.3	616	1 SPAN_STRPU	P98068 strongyloce
4	169	9.1	986	1 NRPI_HUMAN	P13497 homo sapien
5	169	9.1	991	1 NRPI_MOUSE	P98063 mus musculu
6	164.5	8.9	931	1 NRPI_HUMAN	O50462 homo sapien
7	163.5	8.8	922	1 NRPI_RAT	Q9QW19 rattus norv
8	163	8.8	925	1 NRPI_RAT	O35276 rattus norv
9	162.5	8.7	926	1 NRPI_MOUSE	O35251 rattus norv
10	160.5	8.6	923	1 NRPI_MOUSE	P97333 mus musculu
11	160.5	8.6	931	1 NRPI_MOUSE	O35375 mus musculu
12	159	8.6	1022	1 TLD_BRARE	O57460 brachydanio
13	158.5	8.5	923	1 NRPI_HUMAN	O14786 homo sapien
14	157	8.4	914	1 NRPI_CHICK	P79795 gallus gall
15	154	8.3	449	1 PCO1_HUMAN	Q15113 homo sapien
16	148.5	8.0	1057	1 TLD_DROME	P25723 drosophila
17	147	7.9	354	1 NRPI_HUMAN	O43915 homo sapien
18	143.5	7.7	686	1 NRPI_HUMAN	O00187 homo sapien
19	140	7.5	358	1 NRPI_MOUSE	P97946 mus musculu
20	139.5	7.5	597	1 NRPI_MOUSE	P42674 paracentrot
21	138.5	7.5	704	1 NRPI_MOUSE	P98064 mus musculu
22	138	7.4	639	1 NRPI_MOUSE	P98069 strongyloce
23	138	7.4	705	1 NRPI_MOUSE	P00736 homo sapien
24	137.5	7.4	699	1 NRPI_MOUSE	P48740 h complemen
25	132	7.1	419	1 NRPI_MOUSE	P49767 homo sapien
26	128	6.9	468	1 NRPI_MOUSE	Q61398 mus musculu
27	128	6.9	468	1 NRPI_MOUSE	O98628 rattus norv
28	125	6.7	213	1 NRPI_MOUSE	P34007 oryctolagus
29	125	6.7	415	1 NRPI_MOUSE	P97953 mus musculu
30	123.5	6.6	277	1 NRPI_MOUSE	P98066 homo sapien
31	120.5	6.5	245	1 NRPI_MOUSE	P12919 felis silve
32	120.5	6.5	275	1 NRPI_MOUSE	O98859 mus musculu
33	118.5	6.4	276	1 NRPI_MOUSE	P98065 oryctolagus

#### RESULT 1

ID	NRPI_XENLA	STANDARD;	PRT;	928 AA.
AC	P28824;			
DT	01-DEC-1992 (Rel. 24, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Neuropilin-1 precursor (A5 protein) (A5 antigen).			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8395;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=91337458; PubMed=1908252;			
RA	Takagi S, Hirata T, Agata K, Mochii M, Eguchi G, Fujisawa H;			
RT	"The A5 antigen, a candidate for the neuronal recognition molecule,			
RL	Neuron 7:295-307(1991).			
CC	- - FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE			
CC	CERTAIN NEURONAL CIRCUITS, IN ANGIOGENESIS, IN THE FORMATION OF			
CC	SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY			
CC	SIMILARITY). PRESUMED TO BE INVOLVED IN THE NEURONAL RECOGNITION			
CC	BETWEEN THE OPTIC NERVE FIBERS AND THE VISUAL CENTERS.			
CC	- - SUBCELLULAR LOCATION: Type I membrane protein.			
CC	- - TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER			
CC	NEURONS.			
CC	- - SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.			
CC	- - SIMILARITY: Contains 2 CUB domains.			
CC	- - SIMILARITY: Contains 2 F5/8 type C domains.			
CC	- - SIMILARITY: Contains 1 MAM domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
CC	EMBL; D10467; BAA01260.1; -.			
CC	HSSP; P12259; 1C2T.			
DR	InterPro: IPR000859; CUB domain.			
DR	InterPro: IPR000421; FAS8 C.			
DR	InterPro: IPR000998; MAM domain.			
DR	Pfam; PF00431; CUB; 2.			
DR	Pfam; PF00754; F5 F8 type C; 2.			
DR	Pfam; PF00629; MAM; 1.			
DR	PRINTS; PR00020; MAMDOMAIN.			
DR	SMART; SM00042; CUB; 2.			
DR	SMART; SM00231; FAS8C; 2.			
DR	SMART; SM00137; MAM; 1.			
DR	PROSITE; PS01180; CUB; 2.			

P52585 orf virus (

P01127 homo sapien

P13698 xenopus lae

P42664 xenopus lae

P20033 mus musculu

P28576 rattus norv

P26617 cavia porce

P01128 simian sarc

P49765 homo sapien

P13692 homo sapien

P04085 homo sapien

P52584 orf virus (

#### ALIGNMENTS

34 114.5 6.2 148 1 VEGH\_ORFN7

35 114.5 6.2 241 1 PDGB\_HUMAN

36 112.5 6.1 226 1 PDGA\_XENLA

37 111.5 6.0 514 1 UVS2\_XENLA

38 110 5.9 211 1 PDGA\_MOUSE

39 109 5.9 204 1 PDGA\_RAT

40 108.5 5.8 164 1 VEGA\_CAVPO

41 108.5 5.8 226 1 TSIS\_SMSAV

42 105.5 5.7 207 1 VEGH\_HUMAN

43 104.5 5.6 232 1 VEGA\_HUMAN

44 104 5.6 211 1 PDGA\_HUMAN

45 102.5 5.5 133 1 VEGH\_ORFN2



```

DR PROSITE; PS01285; FA58C 1; 2.
DR PROSITE; PS01286; FA58C 2; 2.
DR PROSITE; PS00022; FA58C 3; 2.
DR PROSITE; PS00740; MAM 1; 1.
DR PROSITE; PS00060; MAM 2; 1.
KW Receptor; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 928
FT DOMAIN 22 860
FT TRANSMEM 861 883
FT DOMAIN 884 928
FT DOMAIN 27 141
FT DOMAIN 147 265
FT DOMAIN 275 424
FT DOMAIN 431 584
FT DOMAIN 646 812
FT DISULFID 27 54
FT DISULFID 82 104
FT DISULFID 147 173
FT DISULFID 206 228
FT DISULFID 275 424
FT DISULFID 431 584
FT CARBOHYD 150 150
FT CARBOHYD 261 261
FT CARBOHYD 300 300
FT CARBOHYD 523 523
FT CARBOHYD 844 844
SQ SEQUENCE 928 AA; 103416 MW; AF6B32380A4C789D CRC64;

Query Match 9.7%; Score 179.5; DB 1; Length 928;
Best Local Similarity 31.6%; Pred. No. 2e-07;
Matches 55; Conservative 29; Mismatches 73; Indels 17; Gaps 7;

QY 50 ITVSTNGSIHSPRPHTYPRNTVLVRLVAVEENVWLTDEFGLEDDEDDICKYDFV 109
DB 31 IKITSPSYLSAGVPHSPYPPSQRCWLIQAPEHYQVRIMENPHFDLEDRE--CKYDYV 87

QY 110 EV--EPPSDGILGRWCGSGVPGKQISKQIRIRFVSDYFPPSEPGFCIHYNVMP-- 165
DB 88 EVIDGDNANGQLLKYCKCK-TAPSLVSTGSIPIRVSDYETPG-AGFSIRYEVFTGP 145

QY 166 ----QFTEA--VSPSVLPSPALPDLNNATATSTLEDLIRYLEPERWQDLDE 213
DB 146 ECSRFTSSNGVKSPPYKPYNALECTYIFAPKQOEIV--LEFESFELEAD 197

RESULT 2
BMP1_XENLA
ID BMP1_XENLA STANDARD; PRT; 707 AA.
AC P98070;
DT 01-FEB-1996 (Rel. 33; Created)
DT 01-FEB-1996 (Rel. 33; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8135;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RX MEDLINE=94085787; PubMed=8262384;
RA Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;
RT "Cloning and expression of cDNA encoding Xenopus laevis bone
RT morphogenetic protein-1 during early embryonic development.";
RL Gene 134:257-261(1993).
CC -!- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER
CC DIFFERENTIATION OF DEVELOPING ORGANS.
CC -!- DEVELOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED
CC TADPOLES; LITTLE OR NO EXPRESSION IN MORULA AND LATE GASTRULA.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.

CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 3 CUB domains.
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CC EMBL; LI2249; AAL16313.1; -.
CC PIR; JC2218; JC2218.
CC HSSP; P00736; LAPQ.
CC MEROPS; M12.005; -.
CC InterPro; IPR001506; Astacin.
CC InterPro; IPR000152; Asx_hydroxyl.
CC InterPro; IPR000859; CUB domain.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR006026; NZn_Mtpeptidse.
CC InterPro; IPR006025; Zn_Mtpeptidse.
CC Pfam; PF01400; Astacin; 1.
CC Pfam; PF00431; CUB; 3.
CC Pfam; PF00008; EGF; 1.
CC PRINTS; PR00480; ASTACIN.
CC SMART; SM00042; CUB; 3.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00235; ZNMG; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC PROSITE; PS01180; CUB; 3.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00022; EGF_1; FALSE_NEG.
CC PROSITE; PS00186; EGF_2; 1.
CC PROSITE; PS01187; EGF_CA; 1.
KW Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; Protease;
KW Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
KW Glycoprotein.
FT SIGNAL 1 ?
FT PROPEP ? 83
FT CHAIN 84 707
FT DOMAIN 84 284
FT DOMAIN 285 397
FT DOMAIN 398 509
FT DOMAIN 510 551
FT DOMAIN 554 666
FT METAL 176 176
FT ACT_SITE 177 177
FT METAL 180 180
FT METAL 186 186
FT DISULFID 146 149
FT DISULFID 514 526
FT DISULFID 522 535
FT DISULFID 537 550
FT CARBOHYD 62 62
FT CARBOHYD 105 105
FT CARBOHYD 295 295
FT CARBOHYD 326 326
FT CARBOHYD 562 562
SQ SEQUENCE 707 AA; 80673 MW; 1B6980D716DC9B8D CRC64;

Query Match 9.5%; Score 176; DB 1; Length 707;
Best Local Similarity 43.3%; Pred. No. 2.9e-07;
Matches 45; Conservative 15; Mismatches 36; Indels 8; Gaps 5;

QY 55 NGSIHSPRPHTYPRNTVLVRLVAVEENVWLTDEFGLEDDEDDICKYDFVEVEE- 113
DB 562 NGSINSGPGEKPEYPPNKNCIWLVAPTK-QYRISLKFQ--FETEGNDCKYDFVEVRSG 617

QY 114 -PSDGTILGRWCGSGVPGKQISKQIRIRFVSDYFPPSEPGF 156
DB 618 L7SDSKLHGKFCGS-ELPAVITSQYNNMRIRFKSDNTV-SKKGF 659

```

RESULT 3  
 SPAN STRPU STANDARD; PRT; 616 AA.  
 ID SPAN STRPU STANDARD; PRT; 616 AA.  
 AC P98068;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE SPAN protein precursor (EC 3.4.24.-).  
 GN SPAN.  
 OS Strongylocentrotus purpuratus (Purple sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinozoa; Echinoidae; Echinacea; Echinoida; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 OX NCBI\_TaxID=7668;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=923115921; PubMed=1618141;  
 RA Reynolds S.D., Angerer L.M., Palia J., Nasir A., Angerer R.C.;  
 RT "Early mRNAs, spatially restricted along the animal-vegetal axis of  
 sea urchin embryos, include one encoding a protein related to tollid  
 and BMP-1.";  
 RL Development 114:769-786(1992).  
 CC -!- TISSUE SPECIFICITY: ASYMMETRICALLY ALONG THE ANIMAL-VEGETAL AXIS  
 OF THE BLASTULA.  
 CC -!- DEVELOPMENTAL STAGE: VERY EARLY BLASTULA (BETWEEN 16-CELL STAGE  
 AND HATCHING).  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.  
 CC -!- SIMILARITY: Contains 1 EGF-like domain.  
 CC -!- SIMILARITY: Contains 2 CUB domains.  
 CC  
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 CC  
 CC EMBL; M84144; AAA30072.1; -;  
 DR HSP; P28825; 1IAF.  
 DR MEROPS; M12.013; -;  
 DR InterPro; IPR001506; Astacin.  
 DR InterPro; IPR000859; CUB domain.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR006026; Zn.Mtpeptidse.  
 DR InterPro; IPR006025; Zn.Mtpeptidse.  
 DR Pfam; PF01400; Astacin; 1.  
 DR Pfam; PF00431; CUB; 2.  
 DR PRINTS; PR00480; ASTACIN.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00235; ZnMC; 1.  
 DR PROSITE; PS00142; ZINC PROTEASE; 1.  
 DR PROSITE; PS01180; CUB; 2.  
 DR PROSITE; PS00022; EGF; 1.  
 DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 KW Developmental protein; Repeat; Hydrolase; Protease; Zinc; Embryo;  
 KW Metalloprotease; EGF-like domain; Signal.  
 FT SIGNAL 1 16  
 FT PROPEP 17 93  
 FT CHAIN 94 616  
 FT DOMAIN 89 93  
 FT DOMAIN 94 295  
 FT DOMAIN 295 329  
 FT DOMAIN 340 450  
 FT DOMAIN 451 502  
 FT DOMAIN 503 614  
 FT METAL 190 190  
 FT ACT SITE 191 191  
 FT METAL 194 194  
 FT METAL 200 200  
 FT METAL 200 200

FT DISULFID 299 315 BY SIMILARITY.  
 FT DISULFID 305 317 BY SIMILARITY.  
 FT DISULFID 319 328 BY SIMILARITY.  
 SQ SEQUENCE 616 AA; 67902 MW; 397CD923PFB9EB98 CRC64;  
 Query Match 9.3%; Score 173.5; DB 1; Length 616;  
 Best Local Similarity 27.0%; Pred. No. 3.9e-07;  
 Matches 70; Conservative 33; Mismatches 93; Indels 63; Gaps 14;  
 QY 56 GSIHSPFPHTYPRNTVLVRLVAEENVMVLTQTFDERFGLDEPDDICKYDFVEVEEPS 115  
 Db 349 GRITSPNPSNVEDNTACVYIEGPGYST-IELTF--LDMETETLCRYDAVEVRKDD 404  
 QY 116 DDTILGRMGSGTVPKQISKGNQIRIRFVSDEYFPP--EPGFCIHYNIVMQPTEAVSP 173  
 Db 405 INSIGKFCGN-TLPVPQISSNQMVSTSD---PSITRGRKATVVI--QTTTTFST 459  
 QY 174 SVL---PPSALPLDLLNNAITAFSTLEDLIRYLEPERMQLDLEDLYRPTWOLGKAFVFG 230  
 Db 460 TTLQTPPTSTTLTQTNFSTTLQI-----TNPSTTLTQTD--TPVIGSCGTFV-G 509  
 QY 231 RKSRRVDNLLTEVRLVYSCTPRFSVIR-----ELKSTDTIF-----W 271  
 Db 510 VEGRVASPNY-----PNYDINSLOQDYVIEDGRVRLIFEDFGLEDETTICRW 558  
 QY 272 PGCLL-----VKRCG 281  
 Db 559 DSLMINLNGIKVGMKCG 577  
 RESULT 4  
 BMP1 HUMAN  
 ID BMP1 HUMAN STANDARD; PRT; 986 AA.  
 AC P13497; Q13292; Q13872; Q14874; Q99421; Q99422; Q99423; Q9UL38;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)  
 DE (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mTld).  
 GN BMP1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM BMP1-3).  
 RX TISSUE=Skin;  
 RX MEDLINE=96209868; PubMed=8643539;  
 RA Li S.W., Sieron A.L., Fertala A., Hojima Y., Arnold W.V.,  
 RA Prockop D.J.;  
 RT "The C-proteinase that processes procollagens to fibrillar collagens  
 is identical to the protein previously identified as bone morphogenic  
 protein-1.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM BMP1-1).  
 RX MEDLINE=89072730; PubMed=3201241;  
 RA Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J.,  
 RA Kriz R.W., Hewick R.M., Wang E.A.;  
 RT "Novel regulators of bone formation: molecular clones and  
 activities.";  
 RT Science 242:1528-1534(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6).  
 RX TISSUE=Placenta;  
 RX MEDLINE=98160316; PubMed=9500680;  
 RA Janitz M., Heiser V., Boettcher U., Landt O., Lauter R.;  
 RT "Three alternatively spliced variants of the gene coding for the human  
 bone morphogenetic protein-1.";  
 RN J. Mol. Med. 76:141-146(1998).  
 RN [4]  
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BMP1-3 AND BMP1-7).  
 RX TISSUE=Placenta;



AL)	aps	5;
AL)	EEVE	113
	EVRS	658

Db 659 GLTADSKLHGKFGCS-EKPEVITSQYNMRVFKSDNTV-SKKGFKAHF 705

## RESULT 6

NRP2\_HUMAN STANDARD; PRT; 931 AA.  
 ID NR2P2\_HUMAN STANDARD; PRT; 931 AA.  
 AC O60462; O14820; O14821;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2)  
 GN NR2P2 OR VEGF16SR2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).  
 RX MEDLINE=97470888; PubMed=9331348;  
 RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;  
 RT "Neuropilin-2, a novel member of the neuropilin family, is a high affinity receptor for the semaphorins Sema E and Sema IV but not Sema III.";  
 RL Neuron 19:547-559(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM A22).  
 RC TISSUE=Brain;  
 RX MEDLINE=9818099; PubMed=9529250;  
 RA Soker S., Takahama S., Miao H.-Q., Neufeld G., Klagsbrun M.;  
 RT "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor.";  
 RL Cell 92:735-745(1998).  
 RN [3]  
 RP CHARACTERIZATION.  
 RX MEDLINE=20309748; PubMed=10748121;  
 RA Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;  
 RT "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid form of vascular endothelial growth factor (VEGF) and of placenta growth factor-2, but only neuropilin-2 functions as a receptor for the 145-amino acid form of VEGF.";  
 RL J. Biol. Chem. 275:18040-18045(2000).  
 CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165 AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.  
 CC -!- SUBUNIT: NEUROFILIN-2 PROBABLY FORMS A HETEROMERIC COMPLEX WITH NEUROFILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C RECEPTOR.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=A22;  
 CC IsoId=O60462-1; Sequence=Displayed;  
 CC Name=A0;  
 CC IsoId=O60462-2; Sequence=VSP\_004342;  
 CC Name=A17;  
 CC IsoId=O60462-3; Sequence=VSP\_004341;  
 CC -!- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.  
 CC -!- SIMILARITY: Contains 2 CUB domains.  
 CC -!- SIMILARITY: Contains 2 F5/8 type C domains.  
 CC -!- SIMILARITY: Contains 1 MAM domain.  
 CC -----  
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 CC -----  
 CC ENBL; AF022859; AAC51788.1; -;  
 CC ENBL; AF022860; AAC51789.1; -;  
 CC ENBL; AF016098; AAC12922.1; -;  
 CC HSPF; F12259; ICDT.  
 CC Genew; HGNC:8005; NRP2.

DR MIM; 602070; -. C:membrane fraction; TAS.  
 DR GO; GO:0005624; -. C:membrane fraction; TAS.  
 DR GO; GO:0004872; P:receptor activity; TAS.  
 DR GO; GO:0005021; P:vascular endothelial growth factor receptor. . .; TAS.  
 DR GO; GO:0007411; P:axon guidance; TAS.  
 DR InterPro; IPR000859; CUB domain.  
 DR InterPro; IPR000421; FAS8\_C.  
 DR InterPro; IPR000998; MAM domain.  
 DR Pfam; PF00431; CUB; 2.  
 DR Pfam; PF00754; F5 F8 type C; 2.  
 DR PRINTS; PR00629; MAM; 1.  
 DR PRINTS; PR00020; MAMDOMAIN.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00231; FAS8C; 2.  
 DR SMART; SM00137; MAM; 1.  
 DR PROSITE; PS01180; CUB; 2.  
 DR PROSITE; PS01285; FAS8C\_1; 2.  
 DR PROSITE; PS01286; FAS8C\_2; 2.  
 DR PROSITE; PS00022; FAS8C\_3; 2.  
 DR PROSITE; PS00060; MAM\_2; 1.  
 DR Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;  
 KW Alternative splicing.  
 FT SIGNAL 1 20 OR 22 (POTENTIAL).  
 FT CHAIN 21 931 NEUROFILIN-2.  
 FT DOMAIN 21 864 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 865 889 POTENTIAL.  
 FT DOMAIN 890 931 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 28 142 CUB 1.  
 FT DOMAIN 149 267 CUB 2.  
 FT DOMAIN 277 427 F5/8 TYPE C 1.  
 FT DOMAIN 434 592 F5/8 TYPE C 2.  
 FT DOMAIN 642 802 MAM.  
 FT DOMAIN 671 674 POLY-SER.  
 FT DISULFID 28 55 BY SIMILARITY.  
 FT DISULFID 83 105 BY SIMILARITY.  
 FT DISULFID 149 175 BY SIMILARITY.  
 FT DISULFID 208 230 BY SIMILARITY.  
 FT DISULFID 277 427 BY SIMILARITY.  
 FT DISULFID 434 592 BY SIMILARITY.  
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 839 839 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 809 813 Missing (in isoform A17).  
 FT VARSPLIC 809 830 Missing (in isoform A0).  
 FT CONFLICT 502 602 E -> K (IN REF. 1).  
 FT SEQUENCE 931 AA; 104830 MW; 270CBAB69A0A797C CRC64;  
 Query Match 8.9%; Score 164.5; DB 1; Length 931;  
 Best Local Similarity 29.9%; Pred. No. 3.9e-06;  
 Matches 49; Conservative 20; Mismatches 70; Indels 25; Gaps 5;  
 QY 1 MSLFGLLVTSALAGQRRGTQAEISLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
 Db 1 MDMPFLTWVFLAL-----YFSHQVGRGQDPDPPCGRLNSKDGAYITS 42  
 QY 61 PRFPHYPTNTVLYVRLVAEENYWIQLTFDEREGLEDPPDDICKYDFVEVE--EPSDGT 118  
 Db 43 FGYPQDPYSHQNCWEIVYVPEPNQKIVLNFNPFHEIEKHD---CKYDFIEIRDGDSAD 99  
 QY 119 ILGRCWCSGTVPQKISGKQVIRFVSDYFFSEPGFCIHYNI 162  
 Db 100 LLGKHCNG-IAPPTIISGSMLYIKFTSD-YARQAGAGFSLRYEI 141  
 RESULT 7  
 NRP1\_RAT  
 ID NRPL\_RAT  
 AC Q9QWJ9;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

28-FEB-2003 (Rel. 41, last annotation update)  
 DE Neurophilin-1 precursor (Vascular endothelial cell growth factor 165  
 receptor).  
 GN NRPI.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN  
 [1]  
 SEQUENCE FROM N.A.  
 RP STRAIN=Sprague-Dawley;  
 RC MEDLINE=97433085; PubMed=9288754;  
 RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,  
 RA Ginty D.D.;  
 RT "Neurophilin is a semaphorin III receptor.";  
 RL Cell 90:753-762(1997).  
 CC -!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE  
 CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF  
 CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS  
 CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT  
 CC BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165  
 CC ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN  
 CC INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.  
 CC IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.  
 CC -!- TISSUE SPECIFICITY: FOUND IN THE EMBRYONIC NERVOUS SYSTEM.  
 CC -!- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.  
 CC -!- SIMILARITY: Contains 2 CUB domains.  
 CC -!- SIMILARITY: Contains 2 F5/8 type C domains.  
 CC -!- SIMILARITY: Contains 1 MAM domain.  
 CC  
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 CC  
 CC EMBL; AF016296; AAC53337.1; -.  
 CC HSSP; P12259; 1CZT.  
 CC InterPro; IPR000859; CUB domain.  
 CC InterPro; IPR000421; FAS5 C.  
 CC InterPro; IPR000998; MAM domain.  
 CC Pfam; PF00431; CUB; 2.  
 CC Pfam; PF00754; F5\_F8 type\_C; 2.  
 CC Pfam; PF00629; MAM; 1.  
 CC PRINTS; PR00020; MAMDOMAIN.  
 CC SMART; SM00042; CUB; 2.  
 CC SMART; SM00231; FAS5C; 2.  
 CC SMART; SM00137; MAM; 1.  
 CC PROSITE; PS01180; CUB; 2.  
 CC PROSITE; PS01285; FAS5C.1; 2.  
 CC PROSITE; PS01286; FAS5C.2; 2.  
 CC PROSITE; PS00622; FAS5C.3; 2.  
 CC PROSITE; PS00740; MAM 1; 1.  
 CC PROSITE; PS00660; MAM 2; 1.  
 CC  
 CC Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;  
 KW Receptor.  
 FT SIGNAL 1 21  
 FT CHAIN 22 922  
 FT DOMAIN 22 855  
 FT TRANSMEM 856 880  
 FT DOMAIN 881 922  
 FT DOMAIN 27 141  
 FT DOMAIN 147 265  
 FT DOMAIN 275 424  
 FT DOMAIN 431 583  
 FT DOMAIN 645 811  
 FT DISULFID 27 54  
 FT DISULFID 82 104  
 FT DISULFID 147 173  
 FT DISULFID 206 228





NRP1 MOUSE  
 ID NRP1\_MOUSE STANDARD; PRT; 923 AA.  
 AC P97333;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DT Neuropilin-1 precursor (A5 protein).  
 GN NRP1 OR NRP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Embryonic brain;  
 RA MEDLINE=96353149; PubMed=8748368;  
 RA Kawakami A., Kitsuikawa T., Takagi S., Fujisawa H.;  
 RT "Developmentally regulated expression of a cell surface protein,  
 RT neuropilin, in the mouse nervous system.";  
 RL J. Neurobiol. 29:1-17(1996).  
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE  
 CC CARDIOVASCULAR SYSTEM. IN ANGIOGENESIS, IN THE FORMATION OF  
 CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS  
 CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT  
 CC BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF VEGF, THE VEGF-165  
 CC ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN  
 CC INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.  
 CC IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.  
 CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM.  
 CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.  
 CC -1- SIMILARITY: Contains 2 CUB domains.  
 CC -1- SIMILARITY: Contains 2 F5/8 type C domains.  
 CC -1- SIMILARITY: Contains 1 MAM domain.  
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 CC  
 DR EMBL; D50086; BAA08789.1; -;  
 DR HSP; F12259; ICZT.  
 DR MGD; MGI:106206; NRP.  
 DR InterPro; IPR000859; CUB\_domain.  
 DR InterPro; IPR000421; FA58\_C.  
 DR InterPro; IPR000998; MAM\_domain.  
 DR Pfam; PF00431; CUB; 2.  
 DR Pfam; PF00754; F5\_F8\_type\_C; 2.  
 DR Pfam; PF00629; MAM; 1.  
 DR PRINTS; PR00020; MAMDOMAIN.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00231; FA58C; 2.  
 DR SMART; SM00137; MAM; 1.  
 DR PROSITE; PS01180; CUB; 2.  
 DR PROSITE; PS01285; FA58C\_1; 2.  
 DR PROSITE; PS01286; FA58C\_2; 2.  
 DR PROSITE; PS50022; FA58C\_3; 2.  
 DR PROSITE; PS00740; MAM\_1; 1.  
 DR PROSITE; PS50060; MAM\_2; 1.  
 KW Angiogenesis; Transmembrane; Glycoprotein; Neuron; Signal; Repeat;  
 Receptor.  
 FT SIGNAL 1 21  
 FT CHAIN 22 923  
 FT DOMAIN 22 856  
 FT TRANSMEM 857 879  
 FT DOMAIN 880 923  
 FT DOMAIN 27 141  
 FT DOMAIN 147 265  
 FT DOMAIN 275 424  
 FT DOMAIN 431 583

FT DOMAIN 645 811 MAM.  
 FT DISULFID 27 54 PROBABLE.  
 FT DISULFID 82 104 PROBABLE.  
 FT DISULFID 147 173 PROBABLE.  
 FT DISULFID 206 228 PROBABLE.  
 FT DISULFID 275 424 BY SIMILARITY.  
 FT DISULFID 431 583 BY SIMILARITY.  
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 522 522 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 842 842 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 923 AA; 103020 MW; 064488A170796808 CRC64;  
 Query Match 8.6%; Score 160.5; DB 1; Length 923;  
 Best Local Similarity 36.5%; Pred. No. 8.5e-06;  
 Matches 42; Conservative 16; Mismatches 50; Indels 7; Gaps 4;  
 QY 50 ITVSTNGSIHSPRPHPTNTLVRLVAVENWVIQLTDFERFGLDEPDICKYDV 109  
 Db 31 IKIENPGVLTSPGYSHYHPSEKCEWLIQAEPYQRIIINFNFHFDLEDRD---CKYDV 87  
 QY 110 EV--EPPSGDTILGRWCSGTVPQKISKGNQIRIRFVSDVEYFPSPGFCIHNI 162  
 Db 88 EVIDGENEGRLMKFCGK-IAPSPVSSGPFLLFKVSD-YETHGAGFSIRYEI 140  
 RESULT 11  
 NRP2\_MOUSE STANDARD; PRT; 931 AA.  
 AC O35375; O35373; O35374; O35376; O35377; O35378;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165  
 DE receptor 2).  
 GN NRP2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5).  
 RC STRAIN=BALB/c;  
 RX MEDLINE=97470888; PubMed=9331348;  
 RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;  
 RT "Neuropilin-2, a novel member of the neuropilin family, is a high  
 RT affinity receptor for the semaphorins Sema E and Sema IV but not Sema  
 RT III.";  
 RL Neuron 19:547-559(1997).  
 CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165  
 CC AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.  
 CC -1- SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH  
 CC NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-alternative splicing; Named isoforms=6;  
 CC Name=A22;  
 CC IsoId=O35375-1; Sequence=Displayed;  
 CC Name=A0;  
 CC IsoId=O35375-2; Sequence=VSP\_004344;  
 CC Name=A5;  
 CC IsoId=O35375-3; Sequence=VSP\_004345;  
 CC Name=A17;  
 CC IsoId=O35375-4; Sequence=VSP\_004343;  
 CC Name=B0;  
 CC IsoId=O35375-5; Sequence=VSP\_004346;  
 CC Name=B5;  
 CC IsoId=O35375-6; Sequence=VSP\_004347;  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING CNS, PNS AND IN SOME  
 CC NONNEURAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLES,  
 CC INTESTINAL EPITHELIUM, KIDNEY, LUNG AND SUBMANDIBULAR GLAND.  
 CC -1- DEVELOPMENTAL STAGE: THE EXPRESSION PATTERN IS VERY DYNAMIC AND IS







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CC EMBL; D45416; BAA08256.1; -.
CC HSP; P12259; 1C2T.
CC InterPro; IPR000859; CUB domain.
CC InterPro; IPR000421; FAS8_C.
CC InterPro; IPR000998; MAM_C.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF00754; F5_F8 type C; 2.
CC Pfam; PF00629; MAM; 1.
CC PRINTS; PR00020; MAMDOMAIN.
CC SMART; SM00042; CUB; 2.
CC SMART; SM00231; FAS8C; 2.
CC SMART; SM00137; MAM; 1.
CC PROSITE; PS01180; CUB; 2.
CC PROSITE; PS01285; FAS8C_1; 2.
CC PROSITE; PS01286; FAS8C_2; 2.
CC PROSITE; PS00032; FAS8C_3; 2.
CC PROSITE; PS00740; MAM_1; 1.
CC PROSITE; PS00740; MAM_2; 1.
CC PROSITE; PS00060; MAM_2; 1.
CC Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
KW Receptor; Cell adhesion.
FT SIGNAL 1 18
FT CHAIN 19 914
FT DOMAIN 20 847
FT TRANSMEM 848 870
FT DOMAIN 871 914
FT DOMAIN 25 139
FT DOMAIN 145 263
FT DOMAIN 273 422
FT DOMAIN 429 581
FT DOMAIN 636 801
FT DISULFID 25 52
FT DISULFID 80 102
FT DISULFID 145 171
FT DISULFID 204 226
FT DISULFID 273 422
FT DISULFID 429 581
FT DISULFID 581
SQ SEQUENCE 914 AA; 102480 MW; D02E86DGF0CB68C CRC64;

Query Match 8.4%; Score 157; DB 1; Length 914;
Best Local Similarity 29.4%; Pred. No. 1.7e-05;
Matches 52; Conservative 27; Mismatches 68; Indels 30; Gaps 9;
QY 50 ITVSTGSIHSPFHTYPTNTVLVRLVAVENVMVLTDFEFGLEDDEIDCKYDFV 109
DB 29 IKILSPGLTSPGIFSPSPKQKWLQAPFYQIRIMFNPHFDLEDRD---CKYDYV 85
QY 110 EV--EFPDGTILGRWCGSGTVPGKQISKGNQIRFVSDYFFSEPGFCIHNYVM--P 165
DB 86 EVIDGDNAGRLWKGKCYGK-IAPPLVSGPFLFKFVSD-YETHGAGFIRYEVFKRGP 143
QY 166 Q----FTEAVSPSLP--PSALPLDI-----LNNAITAPSTLLEIRVLEPE 206
DB 144 ECSRNTSSSGMIKSPGFEKYPNSLECTYIIAPKPMSEILFESEFE-----LEPD 195

RESULT 15
PCOL_HUMAN STANDARD; PRT; 449 AA.
AC Q15113; O14550;
CD 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE procollagen C-proteinase enhancer protein precursor (PCPE) (Type I
DE procollagen COOH-terminal proteinase enhancer) (Type I procollagen C-
DE proteinase enhancer protein).
GN PCOLCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
PC SEQUENCE FROM N.A.
PC TISSUE=Placenta;
RX MEDLINE=95014462; PubMed=7523404;
RA Takahara K., Kessler E., Biniaminov L., Brusel M., Eddy R.L.,
RA Jani-Sait S., Shows T.B., Greenspan D.S.;
RT "Type I procollagen COOH-terminal proteinase enhancer protein:
RT identification, primary structure, and chromosomal localization of the
RT cognate human gene (PCOLCE).";
RL J. Biol. Chem. 269:26280-26285(1994).
RN [2]
RN REVISIONS TO 56; 154 AND 373.
RA Kessler E.;
RL Unpublished observations (FEB-2000).
RN [3]
PC SEQUENCE FROM N.A.
PC TISSUE=Heart;
RA Hirahara I., Syoufuda K., Harada K., Tomita M., Urakami K., Terai H.,
RA Morisaki N., Saito Y.;
RT "Smooth muscle cell derived procollagen C-protease enhancer protein.";
RL Cell Struct. Funct. 21:662-662(1996).
RN [4]
PC SEQUENCE FROM N.A.
RX MEDLINE=99018118; PubMed=9799793;
RA Glöckner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,
RA Tsui L.-C., Rosenthal A.;
RT "Large-scale sequencing of two regions in human chromosome 7q22:
RT analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci
RT reveals 17 genes.";
RL Genome Res. 8:1060-1073(1998).
RN [5]
PC SEQUENCE FROM N.A.
PC TISSUE=Placenta;
RX MEDLINE=99134301; PubMed=99333570;
RA Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.;
RT "Structural organization and expression patterns of the human and
RT mouse genes for the type I procollagen COOH-terminal proteinase
RT enhancer protein.";
RL Genomics 55:229-234(1999).
RN [6]
PC SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner I., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzyminski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
PC PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY.
RX MEDLINE=20092917; PubMed=10625689;
RA Mott J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.S.,
RA Banda M.J.;
RT "Post-translational proteolytic processing of procollagen C-terminal
RT proteinase enhancer releases a metalloproteinase inhibitor.";
RL J. Biol. Chem. 275:1384-1390(2000).

```

[illegible]

Search completed: November 25, 2003, 21:02:50  
Job time : 8.55655 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:58:59 ; Search time 30.4613 Seconds  
(without alignments)  
2922.663 Million cell updates/sec

Title: US-09-852-209A-3  
Perfect score: 1858  
Sequence: 1 MSFLGLLVTSALAGRRGT.....DVALEHHHECDVCVRGSGTG 345

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1858	100.0	345	Q9NRA1	Q9nra1 homo sapien
2	1851	99.6	345	Q9UL22	Q9ul22 homo sapien
3	1664	89.6	345	Q9QY71	Q9qy71 mus musculus
4	1662	89.5	345	Q8C119	Q8c119 mus musculus
5	1646	88.6	345	Q9EQX6	Q9eqx6 rattus norv
6	1635	88.0	345	Q9JHV8	Q9jvh8 mus musculus
7	1614	86.9	345	Q9I946	Q9i946 gallus gall
8	1260	67.8	258	Q8K429	Q8k429 rattus norv
9	741.5	39.9	370	Q9GZP0	Q9gzp0 homo sapien
10	740.5	39.9	364	Q9BWV5	Q9bwv5 homo sapien
11	737.5	39.7	370	Q925I7	Q925i7 mus musculus
12	736	39.6	370	Q9EQT1	Q9egt1 rattus norv
13	435.5	23.4	261	Q8K2L3	Q8k2l3 mus musculus
14	190.5	10.3	923	Q8QXK6	Q8qfx6 brachydanio
15	190.5	10.3	923	Q8AXP1	Q8axp1 brachydanio
16	183	9.8	3623	Q60494	Q60494 homo sapien

17	182	9.8	691	13	057658	O57658 gallus gall
18	180	9.7	34	11	Q99JH4	Q99jm4 mus musculus
19	176	9.5	977	13	Q91325	Q91925 xenopus lae
20	176	9.5	3623	11	O70244	O70244 rattus norv
21	172	9.3	1012	11	Q9WVM6	Q9wvm6 mus musculus
22	171	9.2	735	13	O57381	O57381 xenopus lae
23	171	9.2	926	4	Q9UQ00	Q9uq00 homo sapien
24	171	9.2	1015	4	Q9Y6L7	Q9y6l7 homo sapien
25	169	9.1	241	11	Q9Z135	Q9z135 rattus norv
26	165.5	8.9	145	11	Q8BP20	Q8bp20 mus musculus
27	165.5	8.9	926	11	Q8QZY7	Q8qzy7 mus musculus
28	164.5	8.9	555	4	Q9H2E2	Q9h2e2 homo sapien
29	164.5	8.9	901	4	Q9H2E4	Q9h2e4 homo sapien
30	164.5	8.9	901	4	Q9H2D5	Q9h2d5 homo sapien
31	164.5	8.9	906	4	Q9H2D4	Q9h2d4 homo sapien
32	163.5	8.8	906	4	Q9H2E3	Q9h2e3 homo sapien
33	163.5	8.8	921	11	Q9QX38	Q9qx38 rattus norv
34	163.5	8.8	3620	6	Q9TU53	Q9tu53 canis fami
35	161.5	8.7	1007	13	Q8J128	Q8j128 xenopus lae
36	158.5	8.5	609	4	Q96190	Q96190 homo sapien
37	158.5	8.5	644	4	Q961H5	Q961h5 homo sapien
38	158.5	8.5	704	4	Q9H2E1	Q9h2e1 homo sapien
39	157.5	8.5	919	13	Q8UVR0	Q8uvr0 gallus gall
40	157.5	8.5	936	13	Q8UVQ9	Q8uvq9 gallus gall
41	157	8.4	1008	13	Q9DER7	Q9der7 gallus gall
42	153	8.2	415	4	Q9UKZ9	Q9ukz9 homo sapien
43	153	8.2	1019	13	Q57382	O57382 xenopus lae
44	151.5	8.2	326	11	Q91ZE4	Q91ze4 rattus norv
45	151	8.1	276	4	Q9BRH3	Q9brh3 homo sapien

ALIGNMENTS

RESULT 1

Q9NRA1 ID Q9NRA1 PRELIMINARY; PRT; 345 AA.

AC Q9NRA1; DT 01-OCT-2000 (TREMREL. 15, Created)

DT 01-OCT-2000 (TREMREL. 15, Last sequence update)

DT 01-MAR-2003 (TREMREL. 23, Last annotation update)

DE Platelet-derived growth factor C.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI\_TaxID=9606;

RN [1] SEQUENCE FROM N.A.

RP TISSUE=Lung;

RX MEDLINE=20268201; PubMed=10806482;

RA Li X., Ponten A.; Aase K., Karlsson L., Abramson A., Utela M.,

RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,

RA Betsholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U.;

"PDGF-C is a new protease-activated ligand for the PDGF alpha-

RT receptor.";

RL Nat. Cell Biol. 2:302-309(2000).

CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.

DR EMBL; AF244813; AAF80597.1; -

DR InterPro; HGNC:8801; PDGFC.

DR InterPro; IPR000859; CUB domain.

DR Pfam; PF00431; CUB; 1.

DR SMART; SM00042; CUB; 1.

DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS01180; CUB; 1.

DR PROSITE; PS02078; PDGF 2; 1.

SQ SEQUENCE 345 AA; 35043 MW; 590889CEA55CC5EA CRC64;

Query Match 100.0%; Score 1858; DB 4; Length 345;

Best Local Similarity 100.0%; Pred. No. 4.1e-172;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 MSIFGLLLVTSALAGRRGTQAESNLSSKFQSSNKQNGVQDPOHERIITVSTNGSIHS 60  
 DB 1 MSIFGLLLVTSALAGRRGTQAESNLSSKFQSSNKQNGVQDPOHERIITVSTNGSIHS 60  
 QY 61 PRPFHTYPRNTVLVRLVAEENVMQITLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120  
 DB 61 PRPFHTYPRNTVLVRLVAEENVMQITLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120  
 QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPPSEPGFCIHYNIVMPQTEAVSPVLPPSA 180  
 DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPPSEPGFCIHYNIVMPQTEAVSPVLPPSA 180  
 QY 181 LPDLNNAITAPSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240  
 DB 181 LPDLNNAITAPSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240  
 QY 241 LEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300  
 DB 241 LEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300  
 QY 301 VTKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSGG 345  
 DB 301 VTKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSGG 345

## RESULT 2

ID Q9UL22 PRELIMINARY; PRT; 345 AA.  
 AC Q9UL22;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Secretory growth factor-like protein FALLOTEIN (SPINAL CORD-derived growth factor) (Platelet-derived growth factor C).  
 GN RSCDGF OR PDGFC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Tsai Y.-J., Lee R.K.K., Lin S.P.;  
 RT "Falloletin, a novel growth factor like gene identified in human uterus."  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20317014; PubMed=10858496;  
 RA Hamada T., Ui-Tei K., Miyata Y.;  
 RT "A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family."  
 RL FEBS Lett. 475:97-102(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21347863; PubMed=11297552;  
 RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O., Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M., Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;  
 RA "Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor That Binds to PDGF alpha and beta Receptor."  
 RL J. Biol. Chem. 276:27406-27414(2001).  
 CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL; AF091434; AAF00049.1; -.  
 DR EMBL; AB033831; BAB03266.1; -.  
 DR EMBL; AF260738; AAK51637.1; -.  
 DR InterPro: IPR000859; CUB domain.  
 DR InterPro: IPR000072; PD\_growth\_factor.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00341; PDGF; 1.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS0278; PDGF; 2; 1.  
 SQ SEQUENCE 345 AA; 3029 MW; CDE9E51F40633E78 CRC64;  
 Query Match 99.6%; Score 1851; DB 4; Length 345;  
 Best Local Similarity 99.4%; Pred. No. 1.9e-171;  
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSIFGLLLVTSALAGRRGTQAESNLSSKFQSSNKQNGVQDPOHERIITVSTNGSIHS 60  
 DB 1 MSIFGLLLVTSALAGRRGTQAESNLSSKFQSSNKQNGVQDPOHERIITVSTNGSIHS 60  
 QY 61 PRPFHTYPRNTVLVRLVAEENVMQITLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120  
 DB 61 PRPFHTYPRNTVLVRLVAEENVMQITLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120  
 QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPPSEPGFCIHYNIVMPQTEAVSPVLPPSA 180  
 DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPPSEPGFCIHYNIVMPQTEAVSPVLPPSA 180  
 QY 181 LPDLNNAITAPSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240  
 DB 181 LPDLNNAITAPSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240  
 QY 241 LEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300  
 DB 241 LEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300  
 QY 301 VTKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSGG 345  
 DB 301 VTKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSGG 345  
 RESULT 3  
 Q9QY71  
 ID Q9QY71 PRELIMINARY; PRT; 345 AA.  
 AC Q9QY71;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Fallotein (Platelet-derived growth factor C).  
 GN PDGFC.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RA Tsai Y.-J., Lee R.K.K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;  
 RT "cDNA cloning of fallotein from mouse ovary."  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K., Gilbertson D., West J., O'Hara P.J.;  
 RA "Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha receptor."  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cacum, Cerebellum, and Head;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL; AF117608; AAF22516.1; -.  
 DR EMBL; AF266467; AAK58566.1; -.  
 DR EMBL; AK033734; BAC28455.1; -.

Wed Nov 26 13:03:31 2003

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DR EMBL; AK042767; BAC31358.1; -.
DR EMBL; AK052947; BAC35216.1; -.
DR MGI; MGI:1859631; B9gfc.
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF; 2; 1.
DR PROSITE; PS02078; PDGF; 2; 1.
SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;

Query Match      89.6%; Score 1664; DB 11; Length 345;
Best Local Similarity 86.7%; Pred. No. 3e-153;
Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLFGLLVTSALAGQRTGAEANLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MLLGLLLTTSALAGQRTGAEANLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120

QY 61 PKFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120
DB 61 PKFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120

QY 121 GRWCGSGTVPKGKQISKGNQIRIRFVSDEYFSPGFCIHYNIVMPQFTEAVSPSVLPSS 180
DB 121 GRWCGSGTVPKGKQISKGNHIRIRFVSDEYFSPGFCIHYSIIMPQVTTTSPSVLPSS 180

QY 181 LPDLLNNAITAFSTLELIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLELIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240

QY 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
DB 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

QY 301 VTCKYHEVLQRPKTGVRLGKLSLTDVALEHHEECDCVCRGSGTGG 345
DB 301 VTCKYHEVLQRPKTGVRLGKLSLTDVALEHHEECDCVCRGSGTGG 345

Query Match      89.6%; Score 1664; DB 11; Length 345;
Best Local Similarity 86.7%; Pred. No. 3e-153;
Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLFGLLVTSALAGQRTGAEANLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MLLGLLLTTSALAGQRTGAEANLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120

QY 61 PKFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120
DB 61 PKFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120

QY 121 GRWCGSGTVPKGKQISKGNQIRIRFVSDEYFSPGFCIHYNIVMPQFTEAVSPSVLPSS 180
DB 121 GRWCGSGTVPKGKQISKGNHIRIRFVSDEYFSPGFCIHYSIIMPQVTTTSPSVLPSS 180

QY 181 LPDLLNNAITAFSTLELIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLELIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240

QY 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
DB 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

QY 301 VTCKYHEVLQRPKTGVRLGKLSLTDVALEHHEECDCVCRGSGTGG 345
DB 301 VTCKYHEVLQRPKTGVRLGKLSLTDVALEHHEECDCVCRGSGTGG 345

Query Match      89.5%; Score 1662; DB 11; Length 345;
Best Local Similarity 86.4%; Pred. No. 4.7e-153;
Matches 298; Conservative 29; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLFGLLVTSALAGQRTGAEANLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MLLGLLLTTSALAGQRTGAEANLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120

QY 61 PKFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120
DB 61 PKFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120
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QY 121 GRWCGSGTVPKGKQISKGNQIRIRFVSDEYFSPGFCIHYNIVMPQFTEAVSPSVLPSS 180
DB 121 GRWCGSGTVPKGKQISKGNHIRIRFVSDEYFSPGFCIHYSIIMPQVTTTSPSVLPSS 180

QY 181 LPDLLNNAITAFSTLELIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLELIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240

QY 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
DB 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

QY 301 VTCKYHEVLQRPKTGVRLGKLSLTDVALEHHEECDCVCRGSGTGG 345
DB 301 VTCKYHEVLQRPKTGVRLGKLSLTDVALEHHEECDCVCRGSGTGG 345

Query Match      88.6%; Score 1646; DB 11; Length 345;
Best Local Similarity 85.5%; Pred. No. 1.7e-151;
Matches 295; Conservative 30; Mismatches 20; Indels 0; Gaps 0;

QY 1 MSLFGLLVTSALAGQRTGAEANLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MLLGLLLTTSALAGQRTGAEANLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120

QY 121 GRWCGSGTVPKGKQISKGNQIRIRFVSDEYFSPGFCIHYNIVMPQFTEAVSPSVLPSS 180
DB 121 GRWCGSGTVPKGKQISKGNHIRIRFVSDEYFSPGFCIHYSIIMPQVTTTSPSVLPSS 180

QY 181 LPDLLNNAITAFSTLELIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLELIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240

QY 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
DB 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

Query Match      88.6%; Score 1646; DB 11; Length 345;
Best Local Similarity 85.5%; Pred. No. 1.7e-151;
Matches 295; Conservative 30; Mismatches 20; Indels 0; Gaps 0;

QY 1 MSLFGLLVTSALAGQRTGAEANLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MLLGLLLTTSALAGQRTGAEANLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPHYPRNTVLVWRLVAVENVMVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120

QY 121 GRWCGSGTVPKGKQISKGNQIRIRFVSDEYFSPGFCIHYNIVMPQFTEAVSPSVLPSS 180
DB 121 GRWCGSGTVPKGKQISKGNHIRIRFVSDEYFSPGFCIHYSIIMPQVTTTSPSVLPSS 180

QY 181 LPDLLNNAITAFSTLELIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLELIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240

QY 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
DB 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
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Db 241 LKEEVKLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
QY 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHECDVCVCGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHECDVCVCGSTGG 345

RESULT 6
Q9JHV8 Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Platelet-derived growth factor C.
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster/NIH;
EX MEDLINE=20417814; PubMed=10960785;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse Pdgfr gene: dynamic expression in embryonic tissues during
organogenesis.";
RL Mech. Dev. 96:209-213 (2000).
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF286725; AAF91483.1; -.
DR MGD; MG1:1859631; Pdgfc.
DR InterPro; IPR000859; CUB_domain.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 3886 MW; FA1486BED6D362F8 CRC64;

Query Match 88.0%; Score 1635; DB 11; Length 345;
Best Local Similarity 85.5%; Pred. No. 2e-150;
Matches 295; Conservative 28; Mismatches 22; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGQRTQAESNLSSKQFQSSNKQGVQDPQHERIITVSTNGSIHS 60
Db 1 MLLGLLLVTSALAGQRTQAESNLSSKQFQSSNKQGVQDPQHERIITVSTNGSIHS 60
QY 61 PRFPHYPRNTVLVWRLVAEENVMQLTFDERFGLDEPDDICKYDFVEVEPSPDGTIL 120
Db 61 PRFPHYPRNTVLVWRLVAEENVMQLTFDERFGLDEPDDICKYDFVEVEPSPDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPSVLPSPA 180
Db 121 GRWCGSETVPGKQISKGNQIRIRFVSDEYFPPSPGFCIHYSIIMPVTTETSPSVLPSS 180
QY 181 LPDLINNAITASTLEDLIRYLEPERWQDLDELRYRPTWQLGKAFVGRKSRVVDNL 240
Db 181 LSLDLINNAITASTLEDLIRYLEPERWQDLDELRYRPTWQLGKAFVYKSKVVDNL 240
QY 241 LTEEVRLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
Db 241 LKEEVKLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
QY 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHECDVCVCGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHECDVCVCGSTGG 345

RESULT 7
Q9I946 Q9I946 PRELIMINARY; PRT; 345 AA.
AC Q9I946

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DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Spinal cord-derived growth factor.
GN SCDGF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Spinal cord;
EX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102 (2000).
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033829; BAB03265.1; -.
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;

Query Match 86.9%; Score 1614; DB 13; Length 345;
Best Local Similarity 83.8%; Pred. No. 2.2e-148;
Matches 289; Conservative 31; Mismatches 25; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGQRTQAESNLSSKQFQSSNKQGVQDPQHERIITVSTNGSIHS 60
Db 1 MLLGLLLVTSALAGRRHGAESDLSSKFSFGAKQGVQDPQHEKIITVTSNGSIHS 60
QY 61 PRFPHYPRNTVLVWRLVAEENVMQLTFDERFGLDEPDDICKYDFVEVEPSPDGTIL 120
Db 61 PRFPHYPRNTVLVWRLVAEENVMQLTFDERFGLDEPDDICKYDFVEVEPSPDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPSVLPSPA 180
Db 121 GRWCGSSVSPSRQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPSVLPSPA 180
QY 181 LPDLINNAITASTLEDLIRYLEPERWQDLDELRYRPTWQLGKAFVGRKSRVVDNL 240
Db 181 LPDLINNAITASTLEDLIRYLEPERWQDLDELRYRPTWQLGKAFVGRKSRVVDNL 240
QY 241 LTEEVRLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
Db 241 LKEEVKLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
QY 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHECDVCVCGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHECDVCVCGSTGG 345

RESULT 8
Q8K429 Q8K429 PRELIMINARY; PRT; 258 AA.
ID Q8K429
AC Q8K429
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Platelet-derived growth factor C (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=Sprague-Dawley; TISSUE=Skin;
RA Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;
RT "Platelet Derived Growth Factor C (PDGF-C) Expression in Wound
RT Healing.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF0508348; AA047265.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD_Growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
FT NON_TER 1
FT NON_TER 258
SQ
Query Match 67.8%; Score 1260; DB 11; Length 258;
Best Local Similarity 85.6%; Pred. No. 3.9e-114;
Matches 220; Conservative 25; Mismatches 12; Indels 0; Gaps 0;
QY 42 QDQHERIITVSTNGSIHSPRPHTYPRNTVLVWELVAEENVMQLTFDERFGLDEP 101
Db 1 QDPRHERVITSGNSIHSKPKPHTYPRNTVLVWELVAEENVMQLTFDERFGLDEP 60
QY 102 DICKYDFVEVEPSPDITLGRWCGSGTVPKGQISKGNQIRIRFVSDYFPPSPGFCIHY 161
Db 61 DUCKYDFVEVEPSPDITLGRWCGSGTVPKGQISKGNHIRIRFVSDYFPPSPGFCIHY 120
QY 162 IVMPOFTRAVSPVLPPSALPLDNLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWQ 221
Db 121 IIMPQVTTSPVLPPSALSLLDNLNNAITAFSTVEELIRFLEPDWQIDLSLYKPTWP 180
QY 222 LLGKAFVGRKRVVDNLITTEVRLYSCTPNFSVIREELKRTDTTFWPGCLLVKRCG 281
Db 181 LLGKAFVGRKRVVDNLITTEVRLYSCTPNFSVIREELKRTDTTFWPGCLLVKRCG 240
QY 282 GNCACCLHNCNQCQVP 298
Db 241 GNCACCLHNCNQCQVP 257
QY 298 GNCACCLHNCNQCQVP 257
Db 241 GNCACCLHNCNQCQVP 257
RESULT 9
Q9GZP0
ID Q9GZP0 PRELIMINARY; PRT; 370 AA.
AC Q9GZP0.
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE SPINAL CORD-derived growth factor-B (MSTP036) (IRIS-expressed growth
DE factor long form) (Platelet-derived growth factor D).
GN HSCDGF-B OR IEGF OR PDGFD.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
RT SCDFG/PPGF-C/fallotectin.";
RL Biochem. Biophys. Res. Commun. 0:0-0 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;

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RA Wistow G.;
RT "Iris-expressed Growth Factor (IEGF).";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed-11331881;
RA Bergsten E., Urcela M., Li X., Pietras K., Ostman A., Heldin C.H.,
RA Alitalo K., Eriksson U.;
RA "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
RT receptor.";
RN Nat. Cell Biol. 3:512-516(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE-21231380; PubMed-11331882;
RA LaRoche W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J.,
RA Shinkets R.A., Rothberg J.M., Lichenstein H.S.;
RT "PDGF D, A Novel Protease-Activated Growth Factor.";
RN Nat. Cell Biol. 3:517-521(2001).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033832; BAB18903.1; -.
DR EMBL; AF113216; AAG39287.1; -.
DR EMBL; AY027517; AAK20081.1; -.
DR EMBL; AF336376; AAK56136.1; -.
DR EMBL; AF335584; AAK38840.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD growth factor.
DR InterPro; IPR000531; TonB_boxC.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
SQ SEQUENCE 370 AA; 42584 MW; D387F465E7BB7674 CRC64;
Query Match 39.9%; Score 741.5; DB 4; Length 370;
Best Local Similarity 43.6%; Pred. No. 1.6e-63;
Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;
QY 3 LFGLLVTSALAGQRGTQAEENLSKQFSSN---KEQNGVOD-POHERIITVSTNGSI 58
Db 5 IFVYTHICANFCSDRTSATPOSASIKALRNAMLRDENHLLTDLRRDETIOVKNGYV 64
QY 59 HSPRPHTYPRNTVLVWELVAEENVMQLTFDERFGLDEPDDICKYDFVEVEPSPDGT 118
Db 65 QSPRFNSYPRNLLTWRLHS-QENTRIQLVFDNQFGLSEAENDICKYDFVEVEDSETS 123
QY 119 --ILGRWCGSGTVPKGQISKGNQIRIRFVSDYFPPSPGFCIHYNVMPQFTAV---- 171
Db 124 TIIRGERWCGHKEVPPRIKSRNTNQIKITFKSDDYFVAKPGPKIYYSL-LEDFOFAAASETN 182
QY 172 -----SPSVLPSPALPLDNLNNAITAFSTLEDLIRYLEPERWQLDLELYR 217
Db 183 WESVTSSISGVSYNSVSTVDTPT-LIADALDKKTAEDTVEDLLKYFNPSQESQEDLENNYL 241
QY 218 PTWQLLGKAFVGRKRVVDNLITTEVRLYSCTPNFSVIREELKRTDTTFWPGCLLV 277
Db 242 DTPRYGRSY-HDRKSK-VDLDRLNDADAKRYSCTPNYSVNIIEELKLANVWPPRCCLV 299
QY 278 KRCGNCACCLHNCNQCQVPKVKYKHYEVLQIRP---KTGVRGLHKSITDVALEHHEE 334
Db 300 QRCGNCGCGTGVNWRSCNCGTKVTKYKHYEVLQIRP---KTGVRGLHKSITDVALEHHEE 359
QY 335 CDCVC 339
Db 360 CDCIC 364
RESULT 10
Q9BWV5
ID Q9BWV5 PRELIMINARY; PRT; 364 AA.

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AC Q92517; 2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 23, Last annotation update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DE Iris-expressed growth factor short form (Spinal cord-derived growth factor-B).  
 DE factor-B).  
 GN IEGF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Iris;  
 RA Wistow G.;  
 RT "Iris-expressed Growth Factor (IEGF).";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Strausberg K.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY027518; AAK20082.1; -;  
 DR EMBL; BC030645; AAH30645.1; -;  
 DR InterPro; IPR000859; CUB domain.  
 DR InterPro; IPR000072; PD growth factor.  
 DR InterPro; IPR000531; TonB\_boxC.  
 DR Pfam; PF00431; CUB; 1.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS02078; PDGF 2; 1.  
 DR PROSITE; PS00430; TONB DEPENDENT REC 1; 1.  
 DR PROSITE; PS00430; TONB DEPENDENT REC 1; 1.  
 SQ SEQUENCE 364 AA; 42166 MW; 245C53B8DDEA9EAC CRC64;  
 Query Match 39.9%; Score 740.5; DB 4; Length 364;  
 Best Local Similarity 43.2%; Pred. No. 2e-63;  
 Matches 156; Conservative 61; Mismatches 113; Indels 31; Gaps 9;  
 QY 3 LFGLLVTSALAGQRRGTQAESNLSSKQFSSNKEQGVQDPQHERIITVSTNGSIHSPR 62  
 Db 5 IFVYLLICAFNCSCRTSATPQASIKALRNANLRDDLY--RRDETIOVKNGYVQSPR 62  
 QY 63 FHPTYPRTVLVRLVAVENWVQLTDFERFGLGDPEDDICKYDFVEVEPSPDGT--IL 120  
 Db 63 FPNYSFPRNLLTWRLHS-QENTRIQLVFNQFGLAEANDICRYDFVEVEDISETTIIR 121  
 QY 121 GRWCGSGTPGCKQISKGNQIRIFVSDVEYEPSPGFCIHVNIWPOFTEAV----- 171  
 Db 122 GRWCGHKEVPPPKSRNQIKITFKSDDYFVAKPGFIYSL-LDFQPAASSETNWESV 180  
 QY 172 -----SPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPFRWQLDLELYRPTWQ 221  
 Db 181 TSSISGVSYNSPVSPTDPT-LIADALDKKIAEFDTVEDLLKYPFESWQEDLENNYLDTPR 239  
 QY 222 LIGKAFVFGKSRVDNLLTTEVRLVYSCTPRFSVIRELXRTDTIFWPGCLLYKRCG 281  
 Db 240 YRGRSY-HDRKSK-VLDRLNDKAKRYSCTPRYSVNIREFLKVYVFPFRCLLVQRCG 297  
 QY 282 GNCACCLHNCQCVPSKTKYHVLQLRP---KTGVRGLHKLSTDALEHHEECDCV 338  
 Db 298 GNCGCGTGNWNRSTCNSGKTVKKYHVLQEPGHKRGRAKTAVALVDIQLDHHRCDCI 357  
 QY 339 C 339  
 Db 358 C 358  
 RESULT 11  
 Q92517  
 ID Q92517 PRELIMINARY; PRT; 370 AA.  
 AC Q92517; Q92517;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE platelet-derived growth factor D (18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110003109 product:platelet-derived growth factor D).  
 GN PDGFD.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BA1B/C;  
 RX MEDLINE=21231380; PubMed=11331882;  
 RA LaRoche W.J., Jeffers M., McDonald W.F., Chillakuru R.A., Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C., Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J., Shinkets R.A., Rothberg J.M., Lichtenstein H.S.;  
 RA "PDGF D, A Novel Protease-Activated Growth Factor.";  
 RT Nat. Cell Biol. 3:517-521(2001).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Body;  
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanegaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai T., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;  
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Body;  
 RX MEDLINE=22354893; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Body;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Body;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Body;  
 RX MEDLINE=20459374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Body;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,



Search completed: November 25, 2003, 21:04:33  
Job time : 31.4613 secs

Query Match	10.3%;	Score 190.5;	DB 13;	Length 923;
Best Local Similarity	27.16%;	Pred. No. 2.1e-09;		
Matches	66;	Conservative 29;	Mismatches 95;	Indels 49; Gaps 8;
Qy	5	GLLVTSALAGORRGTQAE	NLSLKPFSSNK	EQGVDPQHERITVTSTNGSIHSRPPF 64
Db	12	GIFLVSALKNDKCDN	-----	IRITSANLYTSPGYP 43
Qy	65	HYTPRNTVLVNRILVAEEN	VNWIQLTFFORFGL	EPEDDICKYDFVEVEPSPD - GTILGR 122
Db	44	VSYPSPQCIWVITAPG	NQRIILNFNPH	EDLEDE--CKDYDEVVRGVNDENQLVGK 100
Qy	123	WCGSGTVPGKQISKGNQ	IRIFVDEDEFP	PEPSPGCIHYNIMP-----OFTAEVSPSVL 176
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 22:28:25 ; Search time 3795.28 Seconds  
(without alignments)  
16556.656 Million cell updates/sec

US-09-852-209A-4

Title:  
Perfect score: 1536  
Sequence: 1 cgggtaattccagttttc.....tgctgatagacagactgga 1536

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb\_ba:

2: gb\_htg:

3: gb\_in:

4: gb\_on:

5: gb\_ov:

6: gb\_pat:

7: gb\_ph:

8: gb\_pl:

9: gb\_pr:

10: gb\_ro:

11: gb\_sts:

12: gb\_sy:

13: gb\_un:

14: gb\_vi:

15: em\_ba:

16: em\_fun:

17: em\_hum:

18: em\_in:

19: em\_mu:

20: em\_on:

21: em\_or:

22: em\_ov:

23: em\_pat:

24: em\_ph:

25: em\_pl:

26: em\_ro:

27: em\_sts:

28: em\_un:

29: em\_vi:

30: em\_htg\_hum:

31: em\_htg\_inv:

32: em\_htg\_other:

33: em\_htg\_mus:

34: em\_htg\_pln:

35: em\_htg\_rod:

36: em\_htg\_nam:

37: em\_htg\_vrt:

38: em\_sy:

39: em\_htgo\_hum:

40: em\_htgo\_mus:

41: em\_htgo\_other:

Prei. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1532.6	99.8	2825	6 AR232022	AR232022 Sequence
3	1532.6	99.8	2849	6 AX047650	AX047650 Sequence
4	1532.6	99.8	2849	6 AX391260	AX391260 Sequence
5	1532.6	99.8	2849	6 AX464152	AX464152 Sequence
6	1532.2	99.8	2152	9 AF244813	AF244813 Homo sapi
7	1531	99.7	3007	6 AF234498	AF234498 Sequence
8	1531	99.7	3007	9 AF091434	AF091434 Homo sapi
9	1511.8	98.4	1804	6 AX739931	AX739931 Sequence
10	1511.8	98.4	1804	9 AF260738	AF260738 Homo sapi
11	1511	98.4	1760	6 AR267280	AR267280 Sequence
12	1511	98.4	1760	6 AR282949	AR282949 Sequence
13	1511	98.4	1760	6 AX044518	AX044518 Sequence
14	1511	98.4	1760	6 AX118785	AX118785 Sequence
15	1352.6	88.1	1817	9 AB033831	AB033831 Homo sapi
16	1149	74.8	1328	6 BD004757	BD004757 Novel VRG
17	1149	74.8	1328	6 BD168832	BD168832 Antibody
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19	952.6	62.0	1035	6 AX027935	AX027935 Sequence
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24	721	46.9	3571	6 AX118787	AX118787 Sequence
25	719.4	46.8	2692	10 AF117608	AF117608 Mus muscu
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40	283.4	18.5	289	6 AX027970	AX027970 Sequence
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ALIGNMENTS

RESULT 1

AR210624

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Sequence 1 from patent US 6391311.

AR210624

AR210624.1 GI:21513401

Unknown.

Unknown.

1 (bases 1 to 2825)

Ferrara, N. and Kuo, S.S.

Polypeptides having homology to vascular endothelial cell growth

factor and bone morphogenetic protein 1

Patent: US 6391311-A 1 21-MAY-2002;

linear

DNA

2825 bp

PAT 20-JUN-2002



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Db 1841 TAAACTTGTGTCTGCTGATAGGACAGACTGGA 1873  
RESULT 3  
AX047650 2849 bp DNA linear PAT 15-DEC-2000  
LOCUS Sequence 9 from Patent WO0070050.  
DEFINITION AX047650  
ACCESSION AX047650.1 GI:11876693  
VERSION  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Baker, K.P., Chen, J., Ferrara, N., Fong, S., Goddard, A., Gurney, A.L.,  
Hillan, K.J., Kuo, S.S., Tumas, D. and Wood, W.I.  
TITLE Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 0070050-A 9 23-NOV-2000;  
Genentech, Inc. (US)  
FEATURES  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
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BASE COUNT 851 a 528 c 619 g 850 t 1 others  
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Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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Qy 64 GAATTTACTGTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTATCTTATC 123  
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Qy 124 CAGAAATACGGTCTTGTGTATGGAGATTAGTAGCAGTAGGAGAAATGTATGATACAC 183  
Db 487 CAGAAATACGGTCTTGTGTATGGAGATTAGTAGCAGTAGGAGAAATGTATGATACAC 546  
Qy 184 TTACGTTTTCATGAAGATTTGGCTTGAAGACCCAGAGATGACATATGCAAGTAGTATT 243  
Db 547 TTACGTTTTCATGAAGATTTGGCTTGAAGACCCAGAGATGACATATGCAAGTAGTATT 606



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Db	1867	TAACTTGTCTCATGCTGATAGGACACTGGA	1899
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LOCUS	AX464152	2849 bp	DNA linear PAT 16-JUL-2002
DEFINITION	Sequence 285 from Patent WO0140466.		
ACCESSION	AX464152		
VERSION	AX464152.1	GI:21899092	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E., Sherwood, S., Smith, V., Goddard, A., Godowski, P.J., Gurney, A.L., Wood, W.L. and Zhang, Z.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding same		
JOURNAL	Patent: WO 0140466-A 285 07-JUN-2001;		
FEATURES	Genentech Inc. (US)		
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RESULT 6  
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LOCUS AF244813 2152 bp mRNA linear PRI 27-AUG-2001  
DEFINITION Homo sapiens platelet-derived growth factor C mRNA, complete cds.  
ACCESSION AF244813  
VERSION AF244813.1 GI:8886883  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2152)  
AUTHORS Li,X., Ponten,A., Jase,K., Karlsson,L., Abramson,A., Uucela,M., Backstrom,G., Hellstrom,M., Bostrom,H., Li,H., Soriano,P., Besholtz,C., Heldin,C.-H., Allitalo,K., Ostman,A. and Eriksson,U.  
PDGF-C is a new protease-activated ligand for the PDGF alpha-receptor  
Nat. Cell Biol. 2 (5), 302-309 (2000)  
JOURNAL Nat. Cell Biol. 2 (5), 302-309 (2000)  
MEDLINE 20268201  
PUBMED 10806482  
REFERENCE 2 (bases 1 to 2152)  
AUTHORS Eriksson,U., Aase,K., Li,X. and Ponten,A.  
Direct Submission  
TITLE Submitted (14-MAR-2000) Ludwig Institute for Cancer Research,  
JOURNAL Nobels vag 3 P.O.Box 240, Stockholm S-171 77, Sweden  
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ACCESSION AX234498  
VERSION AX234498.1 GI:15593481  
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REFERENCE  
1 Alitalo,K.M. and Jeltsch,M.M.  
Materials and methods involving hybrid vascular endothelial growth  
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JOURNAL LUDWIG INSTITUTE FOR CANCER RESEARCH (US) ; Licentia OY (FI)  
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ACCESSION AF091434  
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REFERENCE  
1 (bases 1 to 3007)  
Tsai, Y.J., Lee, R.K., Lin, S.P. and Chen, Y.H.  
Identification of a novel placenta-derived growth factor-like gene,  
fallotein, in the human reproductive tract  
Biochim. Biophys. Acta 1492 (1), 196-202 (2000)  
JOURNAL  
MEDLINE 20461776  
PUBMED 11004490  
REFERENCE 2 (bases 1 to 3007).  
Tsai, Y.J., Lee, R.K.K. and Lin, S.P.  
Direct Submission  
AUTHORS  
TITLE  
JOURNAL  
Hosptial, 45 Min Sheng Road, Tamsui, Taipei County 25115, Taiwan  
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ACCESSION AF260738  
VERSION AF260738.1 GI:14009503  
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REFERENCE 1 (bases 1 to 1804)  
AUTHORS Gilbertson,D.G., Duff,M.E., West,J.W., Kelly,J.D., Sheppard,P.O.,  
Hofstrand,P.D., Gao,Z., Shoemaker,K., Bukowski,T.R., Moore,M.,  
Feidhaus,A.L., Humes,J.M., Palmer,T.E. and Hart,C.B.  
TITLE Platelet-derived growth factor C (PDGFC), a novel growth factor  
that binds to PDGF alpha and beta receptor  
J. Biol. Chem. 276 (29), 27406-27414 (2001)  
21347863  
PUBMED 11297552  
REFERENCE 2 (bases 1 to 1804)  
AUTHORS Gao,Z., Hart,C., Piddington,C., Sheppard,P., Shoemaker,K.,  
Gilbertson,D., West,J. and O'Hara,P.J.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2000) Biomolecular Informatics, ZymoGenetics,  
Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA  
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DEFINITION Sequence 32 from patent US 6495668.  
ACCESSION AR267280  
VERSION AR267280.1 GI:29697283  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unkown.  
REFERENCE 1 (bases 1 to 1760)  
AUTHORS Gilbert, T., Hart, C.E., Sheppard, P.O. and Gilbertson, D.G.  
TITLE Growth factor homolog ZVGF4  
JOURNAL Patent: US 6495668-A 32 17-DEC-2002;  
FEATURES Location/Qualifiers  
source 1..1760  
BASE COUNT 494 a 373 c 411 g 482 t  
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DEFINITION Sequence 1 from patent US 6528050.  
ACCESSION AR282949  
VERSION AR282949.1 GI:29719770  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1760)  
AUTHORS Gao,Z., Hart,C.E., Piddington,C.S., Sheppard,P.O., Shoemaker,K.E.,  
Gilbertson,P.G. and West,J.W.  
TITLE Growth factor homolog zvegfg3  
JOURNAL Patent: US 6528050-A 1 04-MAR-2003;  
FEATURES Location/Qualifiers  
source 1. 1760  
BASE COUNT 494 a 373 c 411 g 482 t  
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DEFINITION Sequence 1 from Patent WO0128586.  
ACCESSION AX118785

AX118785.1 GI:14035734  
Homo sapiens (human)  
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Method of treating fibrosis  
Patent: WO 0128586-A.1 26-APR-2001;  
Zymogenetics, Inc. (US)  
REFERENCE  
1 Gilbertson, D.G.  
AUTHORS  
TITLE  
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BASE COUNT 494 a 373 c 411 g 482 t  
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Best Local Similarity 99.8%; Pred. No. 0;  
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LOCUS  
DEFINITION Homo sapiens hSCDGF mRNA for spinal cord-derived growth factor,  
complete cds.  
ACCESSION AB033831

VERSION	AB033831.1	GI:9392293
KEYWORDS	spinal cord-derived growth factor; scdgf gene.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	1 (sites)	
AUTHORS	Hamada,T., Ui-Tei,K. and Miyata,Y.	
TITLE	A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family	
JOURNAL	FEBS Lett. 475 (2), 97-102 (2000)	
MEDLINE	20317014	
PUBMED	10858496	
REFERENCE	2 (bases 1 to 1817)	
AUTHORS	Hamada,T., Ui-Tei,K. and Miyata,Y.	
TITLE	Direct Submission	
JOURNAL	Submitted (25-OCT-1999) Tsuyoshi Hamada, Nippon Medical School, Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo 113-8602, Japan (E-mail:t-hamada@nms.ac.jp, Tel:81-3-3822-2131(ex.5277), Fax:81-3-5814-1684)	
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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#### SUMMARIES

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DNA encoding human  
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Human PRO200 (UNQ1  
Human PRO200 (VEGF  
Human PRO200 prote  
Human PRO713 CDNA

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19	1531	99.7	2839	21	AAA7452	Human TANGO 128 co
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21	1531	99.7	3007	22	AAZ12884	DNA encoding for h
22	1529.4	99.6	2779	21	AAZ52458	CDNA encoding huma
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25	1518.4	98.9	2776	21	AAA71952	Human VEGF-X homol
26	1515.8	98.7	2827	22	AAZ06812	Human LPS, a PDGF-
27	1515.8	98.7	2896	21	AAZ64426	Human platelet-der
28	1515.8	98.7	2898	20	AAZ86352	DNA encoding human
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#### ALIGNMENTS

#### RESULT 1

AAA12524

ID AAA12524 standard; CDNA; 1536 BP.

XX

AC AAA12524;

XX

DT 25-JUL-2000 (first entry)

XX

DE CDNA encoding a fragment of platelet-derived growth factor C (PDGF-C).

XX

KW Platelet-derived growth factor C; PDGF-C; cell proliferation;

KW growth factor; heparin; connective tissue; wound healing; VEGF-P;

KW fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;

KW choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;

KW lung carcinoma; erythroleukemia; tissue remodelling; ss.

XX Homo sapiens.

XX

FH Key Location/Qualifiers

CDS 3..959

FT /\*tag= a

FT /product= "platelet-derived growth factor C fragment"

FT /transl\_except= (pos: 861...863, aa: Lys)

XX

XX WO200018212-A2.

XX

XX 06-APR-2000.

XX

XX 30-SEP-1999; 99WO-US22668.

XX

XX 30-SEP-1998; 98US-0102461.

PR 12-NOV-1998; 98US-0108109.  
PR 03-DEC-1998; 98US-0110749.  
PR 18-DEC-1998; 98US-0113002.  
PR 21-MAY-1999; 99US-0135426.  
PR 15-JUL-1999; 99US-0144022.  
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PA (UYHE-) UNIV HELSINKI LICENSING LTD.  
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XX Erikson U, Aase K, Lee X, Ponten A, Uutela M, Alitalo K;  
PI Oestman A, Heidin C, Betsholz C;  
XX  
DR WPI; 2000-292954/25.  
DR P-PSDB; AAY84558.  
XX  
PT Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,  
PT differentiation, growth and motility of cells expressing the PDGF-C  
PT receptor -  
XX  
PS Claim 9; Fig 3; 135pp; English.  
XX  
CC The present sequence encodes a human platelet-derived growth factor C  
CC (PDGF-C) (formally designated VEGF-F) fragment. PDGF-C polypeptides have  
CC the ability to stimulate and enhance proliferation or differentiation,  
CC and/or growth or motility of cells expressing a PDGF-C receptor.  
CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell  
CC proliferation, preferably in combination with one other growth factor  
CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also  
CC be used for stimulating connective tissue or wound healing. The  
CC PDGF-C polypeptide can be enzymatically processed to generate the active  
CC truncated form of PDGF-C and used to regulate the receptor-binding  
CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast  
CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.  
CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour  
CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.  
CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma  
CC and erythroleukemia, can be identified by testing for expression of  
CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue  
CC remodelling during invasion of tumour cells into a normal population of  
CC cells. Antagonists can also be used to treat fibrotic conditions,  
CC especially found in the lung, kidney or liver.  
XX  
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Query Match 100.0%; Score 1535.6; DB 21; Length 1536;  
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DB 181 AACTTAGCTTGTGAAGATTTGGCTTGAAGACCCAGAGATGACATATGCAAGATG 240  
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KW VEGF-E; human; vascular endothelial cell growth factor; wound repair;  
KW treatment; cardiovascular disorder; endothelial disorder; therapy;  
KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;  
KW angiogenic disorder; age-related macular degeneration; vascular disease;  
KW neovascularization; tumor; gene mapping; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 259..1296  
FT FT /\*tag= a  
FT FT /product= "VEGF-E"  
XX  
PN WO9947677-A2.  
XX  
PD 23-SEP-1999.  
XX  
PF 10-MAR-1999; 99WO-US05190.  
XX  
PR 17-MAR-1998; 98US-0040220.  
PR 02-NOV-1998; 98US-0184216.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ferrara N, Kuo SS;  
XX  
XX WPI; 1999-580306/49.  
DR P-PSDB; AAY33679.  
XX  
PT New growth factor polypeptide useful for treating cardiovascular or  
PT endothelial disorders, e.g. cardiac hypertrophy -  
XX  
PS Claim 2; Fig 1; 122pp; English.  
XX  
CC This invention describes the isolation of a novel human vascular  
CC endothelial cell growth factor-E (VEGF-E) polypeptide which has  
CC tranquilizer, vulnery and cardiant activity. VEGF-E can be administered  
CC therapeutically, especially by expressing encoding polynucleotides to  
CC treat cardiovascular or endothelial disorders in mammals, especially  
CC humans. It is useful in wound repair and tissue generation and  
CC regeneration, and may especially be used to treat cardiac hypertrophy  
CC It can be combined with a carrier in pharmaceutical compositions, which  
CC can be administered to treat disorders as above. VEGF-E can be used to  
CC screen for antagonists and agonists, and the antagonists administered to  
CC treat angiogenic disorders in mammals (especially humans) administered to  
CC age-related macular degeneration. It can be used to generate antibodies,  
CC useful therapeutically as antagonists, as above. The antibodies are also  
CC useful to detect VEGF-E polypeptide, especially to diagnose  
CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.  
CC vascular disease, or neovascularization associated with tumor formation),  
CC by contacting the antibody with a tissue sample and detecting formation  
CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding  
CC VEGF-E can be used to diagnose cardiovascular and endothelial disorders  
CC in mammals, by detecting abnormally high or low VEGF-E gene expression in  
CC tissue samples. They can also be used to diagnose a disease or  
CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a

CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by  
CC detecting a mutation in the VEGF-E-encoding sequence isolated from a  
CC sample. They may also be used to produce probes useful to detect related  
CC sequences or for gene mapping. This sequence encodes the human VEGF-E  
CC protein described in the method of the invention.  
XX  
SQ Sequence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;  
Query Match 99.8%; Score 1532.6; DB 20; Length 2825;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GTAATTCAGTTTCCAGCAACAAAGGAACAGACGAGTACCAATCTCTCAGATGAGA 63  
Db 341 GTAAATTCAGTTTCCAGCAACAAAGGAACAGACGAGTACCAATCTCTCAGATGAGA 400  
QY 64 GAAATTTACTGTGTCTACTAATGGAAGTATTCAGGCCCAAGGTTTCTCTACTATTC 123  
Db 401 GAAATTTACTGTGTCTACTAATGGAAGTATTCAGGCCCAAGGTTTCTCTACTATTC 460  
QY 124 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGATACAAAC 183  
Db 461 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGATACAAAC 520  
QY 184 TTACGTTTGTATCAAAAGATTGCGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATGAT 243  
Db 521 TTACGTTTGTATCAAAAGATTGCGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATGAT 580  
QY 244 TTGTAGAAGTTGAGGAACCCAGTAGTGAACCTATATTAGGGCGCTGGTGTCTGCTA 303  
Db 581 TTGTAGAAGTTGAGGAACCCAGTAGTGAACCTATATTAGGGCGCTGGTGTCTGCTA 640  
QY 304 CTGTACCAAGGAAACAGAGATTTCTAAGGAATCAAAATTAGGATAAGATTTGTATCTGATG 363  
Db 641 CTGTACCAAGGAAACAGAGATTTCTAAGGAATCAAAATTAGGATAAGATTTGTATCTGATG 700  
QY 364 AATATTTCTTCTGAACACAGGGTTCTGCATCCACTACAACATTTGTCATGCCAATTCOA 423  
Db 701 AATATTTCTTCTGAACACAGGGTTCTGCATCCACTACAACATTTGTCATGCCAATTCOA 760  
QY 424 CAGAAGCTGTGAGTCTTCACTGCTTACCCCTTCACTTGGCACTGGACCTGCTTAATA 483  
Db 761 CAGAAGCTGTGAGTCTTCACTGCTTACCCCTTCACTTGGCACTGGACCTGCTTAATA 820  
QY 484 ATGCTATAAATGCTCTTGTAGTACCTTTGGAAGACCTTATTTCGATATCTTGAACACAGAGAT 543  
Db 821 ATGCTATAAATGCTCTTGTAGTACCTTTGGAAGACCTTATTTCGATATCTTGAACACAGAGAT 880  
QY 544 GGCAGTTGGACTTGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 603  
Db 881 GGCAGTTGGACTTGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 940  
QY 604 TTTTGGGAAGAAATCCAGAGTGTGGATCTGACCTTCTAACAGAGAGGTAAATAT 663  
Db 941 TTTTGGGAAGAAATCCAGAGTGTGGATCTGAACTTCTAACAGAGAGGTAAATAT 1000  
QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGGATA 723  
Db 1001 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGGATA 1060  
QY 724 CCATTTTCTGCCAGGTTGTCTCTCGTGTAAACGCTGTGGGGAACCTGTGCTGTGTGTC 783  
Db 1061 CCATTTTCTGCCAGGTTGTCTCTCGTGTAAACGCTGTGGGGAACCTGTGCTGTGTGTC 1120  
QY 784 TCCCAATTCGAATGATGTCATGTCCTCCCAACCAAGTTACTAAAAAATACACAGAGG 843  
Db 1121 TCCCAATTCGAATGATGTCATGTCCTCCCAACCAAGTTACTAAAAAATACACAGAGG 1180  
QY 844 TCCTTCTAGTTGAGACCAAAACCGGTGTTCAGGGGATTTGCACAAATCACTACCCACCGTGG 903  
Db 1181 TCCTTCTAGTTGAGACCAAAACCGGTGTTCAGGGGATTTGCACAAATCACTACCCACCGTGG 1240  
QY 904 CCCTGGAGCACCATGAGGAGTGTGATGCTGTGTGTGTCAGAGGGAGCAGAGGATAGCCGC 963

Db 1241 CCCTGGAGCACCATGAGGAGTGTACTGTGTGTCAGAGGAGCAGACGAGGATAGCCGC 1300  
QY 964 ATCCACACAGAGCTCTTGGCCAGAGCTGTGCAGTGCAGTGGCTGATCTTATTAGAGAA 1023  
Db 1301 ATCCACACAGAGCTCTTGGCCAGAGCTGTGCAGTGCAGTGGCTGATCTTATTAGAGAA 1360  
QY 1024 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTTGTCTCAAGACCTTTTCATCTTCAG 1083  
Db 1361 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTTGTCTCAAGACCTTTTCATCTTCAG 1420  
QY 1084 GATTACAGTGCATCTGAAGAGAGAGACATCAACAGAAATTAGAGTTGTGCAACAGCT 1143  
Db 1421 GATTACAGTGCATCTGAAGAGAGAGACATCAACAGAAATTAGAGTTGTGCAACAGCT 1480  
QY 1144 CTTTTTGAGAGGCGCTTAAAGACAGGAGAGAAAGGTCTTCAATCGTGAAGAAATTA 1203  
Db 1481 CTTTTTGAGAGGCGCTTAAAGACAGGAGAGAAAGGTCTTCAATCGTGAAGAAATTA 1540  
QY 1204 ATGTTGTATTAAATAGATCACAGCTAGTTTCAAGATTTACCATGTACCTATTCCATAGC 1263  
Db 1541 ATGTTGTATTAAATAGATCACAGCTAGTTTCAAGATTTACCATGTACCTATTCCATAGC 1600  
QY 1264 TGGGTTCTGTATTTCAGTCTTTCGATACGGCTTAGGCTTAATGTCTAGTACAGGAGAAAA 1323  
Db 1601 TGGGTTCTGTATTTCAGTCTTTCGATACGGCTTAGGCTTAATGTCTAGTACAGGAGAAAA 1660  
QY 1324 CTGTGCAAGTGAGCACCTGATTCCTGCTTAACTCTTAAAGTCCATGTCTCTGG 1383  
Db 1661 CTGTGCAAGTGAGCACCTGATTCCTGCTTAACTCTTAAAGTCCATGTCTCTGG 1720  
QY 1384 CCTAAATCGTAAATCTGATTTTCTGATACCTGCTTTTAAAGAACTATGTTGCTATGAAT 1443  
Db 1721 CCTAAATCGTAAATCTGATTTTCTGATACCTGCTTTTAAAGAACTATGTTGCTATGAAT 1780  
QY 1444 ACCAGACATCTATGTACTACACACCTGCTTTTAAAGAACTATGTTGCTATGAAT 1503  
Db 1781 ACCAGACATCTATGTACTACACACCTGCTTTTAAAGAACTATGTTGCTATGAAT 1840  
QY 1504 TAAACTTGTCATGCTGATGAGCAGACTGGA 1536  
Db 1841 TAAACTTGTCATGCTGATGAGCAGACTGGA 1873

RESULT 3  
ID ABS57294  
AC ABS57294 standard; DNA; 2825 BP.  
XX ABS57294;  
XX 31-JAN-2003 (first entry)  
XX DNA encoding human vascular endothelial cell growth factor-E (VEGF-E).  
DE Human; vascular endothelial cell growth factor-E; VEGF-E; PRO:200;  
XX VEGF; bone morphogenetic protein 1; wound repair; tissue regeneration;  
XX cardiovascular disorder; endothelial disorder; angiogenic disorder;  
XX cancer; diabetes mellitus; cardiac hypertrophy; atherosclerosis;  
XX cardiant; cytosstatic; antidiabetic; antiarteriosclerotic;  
XX gene therapy; gene; ds.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 259..1296  
FT FT /\*tag= a  
FT FT /product= "VEGF-E"  
XX  
PN US8455283-B1.  
XX  
PD 24-SEP-2002.  
XX  
XX 10-MAR-1999; 99US-0265686.  
PF

XX 17-MAR-1998; 98US-0040220.  
PR 02-NOV-1998; 98US-0184216.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ferrara N, Kuo SS;  
XX WPI; 2003-066231/06.  
DR P-PSDB; ABG72132.  
XX  
PT New nucleic acid encoding endothelial cell growth factor-E polypeptide,  
PT useful for diagnosing or treating a cardiovascular, endothelial or  
PT angiogenic disorder such as cancer, diabetes mellitus or  
PT atherosclerosis  
XX  
PS Claim 2; Fig 1; 46pp; English.  
XX  
CC The present invention relates to the isolation of human vascular  
CC endothelial cell growth factor-E (VEGF-E, also referred to as  
CC PRO:200), and the polynucleotide sequence encoding it. VEGF-E is  
CC related to VEGF and bone morphogenetic protein 1. VEGF-E is useful  
CC in wound repair, as well as in the generation and regeneration of  
CC tissue. The sequences of the invention are useful for diagnosing or  
CC treating cardiovascular, endothelial or angiogenic disorders such as  
CC cancer, diabetes mellitus, cardiac hypertrophy and atherosclerosis.  
CC The polynucleotide encoding VEGF-E is useful in the gene therapy of  
CC such disorders. The present sequence encodes human VEGF-E.  
SQ Sequence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;  
Query Match 99.8%; Score 1532.6; DB 25; Length 2825;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GTAAATTCAGTTTCCAGCAACAGGAAACAGACGGAGTACAGATCTCAGCATGAGA 63  
Db 341 GTAAATTCAGTTTCCAGCAACAGGAAACAGACGGAGTACAGATCTCAGCATGAGA 400  
QY 64 GAAATTTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTACTATTATC 123  
Db 401 GAAATTTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTACTATTATC 460  
QY 124 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGATACAAC 183  
Db 461 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGATACAAC 520  
QY 184 TTACGTTTGTGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243  
Db 521 TTACGTTTGTGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 580  
QY 244 TTGTAGAAGTTGAGGAACCCAGTGTATGGAACCTATATTAGGCGCTGGTGTCTGGTA 303  
Db 581 TTGTAGAAGTTGAGGAACCCAGTGTATGGAACCTATATTAGGCGCTGGTGTCTGGTA 640  
QY 304 CTGTACACAGGAAAAACAGATTTCTAAAGAAATCAAAATTAGAATAAGATTGTATCTGATG 363  
Db 641 CTGTACACAGGAAAAACAGATTTCTAAAGAAATCAAAATTAGAATAAGATTGTATCTGATG 700  
QY 364 AATATTTTCTCTGAAACAGGTTTCTGCATCCACTACAACATTTGTCTATGCCACATTCA 423  
Db 701 AATATTTTCTCTGAAACAGGTTTCTGCATCCACTACAACATTTGTCTATGCCACATTCA 760  
QY 424 CAGAAGCTGTGAGTCTCTTCACTGTCTACCCCTTTCAGCTTTTCCACTGTGACCTGTCTAATA 483  
Db 761 CAGAAGCTGTGAGTCTCTTCACTGTCTACCCCTTTCAGCTTTGCCACTGTGACCTGTCTAATA 820  
QY 484 ATGCTATAACCTGCTTTTAGTACCTTGAAGACCTTTATTCGATATCTTGAACACAGAGAT 543  
Db 821 ATGCTATAACCTGCTTTTAGTACCTTGAAGACCTTTATTCGATATCTTGAACACAGAGAT 880  
QY 544 GGCAGTTGGACTTAGAAGTCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 603

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Db      881  GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTG 940
QY      604  TTTTGGAGAAAAATCCAGAGTGGTGGATCTGAACTTCTTAAACAGAGGAGGTAAAGATTAT 663
Db      941  TTTTGGAGAAAAATCCAGAGTGGTGGATCTGAACTTCTTAAACAGAGGAGGTAAAGATTAT 1000
QY      664  ACAGCTGCACACTCGTAACTTCTCAGTGTCCATAGGGAAGAACTATAAGAGAACCGATA 723
Db     1001  ACAGCTGCACACTCGTAACTTCTCAGTGTCCATAGGGAAGAACTATAAGAGAACCGATA 1060
QY      724  CCATTTCTTGGCCAGAGTGTCTCCTGGTTAAAGCGCTGTGTGGGAACTGTGCCCTGTTGTC 783
Db     1061  CCATTTCTTGGCCAGAGTGTCTCCTGGTTAAAGCGCTGTGTGGGAACTGTGCCCTGTTGTC 1120
QY      784  TCCACAATGCAATGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCAAGAGG 843
Db     1121  TCCACAATGCAATGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCAAGAGG 1180
QY      844  TCCTTTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCACAAATCACTCACCGACGTGG 903
Db     1181  TCCTTTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCACAAATCACTCACCGACGTGG 1240
QY      904  CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGAGGATAGCGCG 963
Db     1241  CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGAGGATAGCGCG 1300
QY      964  ATCACACACAGCAGCTCTTGCCAGAGCTGTGTCAGTGCAGTGCAGTGTGATTTATAGAGAA 1023
Db     1301  ATCACACACAGCAGCTCTTGCCAGAGCTGTGTCAGTGCAGTGCAGTGTGATTTATAGAGAA 1360
QY     1024  CGTATCGGTTATCTCCATCTTAATCTCAGTGTGTGCTTCAGGACCTTTTCATCTTCAG 1083
Db     1361  CGTATCGGTTATCTCCATCTTAATCTCAGTGTGTGCTTCAGGACCTTTTCATCTTCAG 1420
QY     1084  GATTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTAGGAGTTGTGCAACAGCT 1143
Db     1421  GATTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTAGGAGTTGTGCAACAGCT 1480
QY     1144  CTTTTCAGAGGAGGCGCTTAAGGACAGAGAAAGGCTTCAATCGTGGAAAGAAATTAA 1203
Db     1481  CTTTTCAGAGGAGGCGCTTAAGGACAGAGAAAGGCTTCAATCGTGGAAAGAAATTAA 1540
QY     1204  ATGTTCTGTTAATATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCTAGC 1263
Db     1541  ATGTTCTGTTAATATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCTAGC 1600
QY     1264  TGGGTTCTGTATTTCAAGTCTTTTCGATACGGCTTAGGGTAATGTCAATCGTGGAAAAAAA 1323
Db     1601  TGGGTTCTGTATTTCAAGTCTTTTCGATACGGCTTAGGGTAATGTCAATCGTGGAAAAAAA 1660
QY     1324  CTGTGCAAGTGAGCACCTGATTCGGTTCCTTGCCTTAACCTTAAGCTCCATGTCTCTGG 1383
Db     1661  CTGTGCAAGTGAGCACCTGATTCGGTTCCTTGCCTTAACCTTAAGCTCCATGTCTCTGG 1720
QY     1384  CCTAAATCGTATAAATCTGAAATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATGTAA 1443
Db     1721  CCTAAATCGTATAAATCTGAAATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATGTAA 1780
QY     1444  ACCAGAACATTTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTGTCTATGAAT 1503
Db     1781  ACCAGAACATTTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTGTCTATGAAT 1840
QY     1504  TAAACTGTGTCTATGTCTATAGACAGACTGGA 1536
Db     1841  TAAACTGTGTCTATGTCTATAGACAGACTGGA 1873
```

RESULT 4

AAZ34296

ID AAZ34296 standard; cDNA; 2849 BP.

XX

AC AAZ34296;

XX

DT 07-DEC-1999 (first entry)  
XX Human PR0200 nucleotide sequence.  
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein; ss.  
XX Homo sapiens.  
XX WO9946281-A2.  
XX 16-SEP-1999.  
XX 08-MAR-1999; 99WO-US05028.  
XX 10-MAR-1998; 98US-0077450.  
XX 11-MAR-1998; 98US-0077632.  
XX 11-MAR-1998; 98US-0077641.  
XX 11-MAR-1998; 98US-0077649.  
XX 12-MAR-1998; 98US-0077791.  
XX 13-MAR-1998; 98US-0078004.  
XX 17-MAR-1998; 98US-0040220.  
XX 20-MAR-1998; 98US-0078886.  
XX 20-MAR-1998; 98US-0078910.  
XX 20-MAR-1998; 98US-0078936.  
XX 20-MAR-1998; 98US-0078939.  
XX 25-MAR-1998; 98US-0079294.  
XX 26-MAR-1998; 98US-0079656.  
XX 27-MAR-1998; 98US-0079663.  
XX 27-MAR-1998; 98US-0079664.  
XX 27-MAR-1998; 98US-0079689.  
XX 27-MAR-1998; 98US-0079728.  
XX 27-MAR-1998; 98US-0079786.  
XX 30-MAR-1998; 98US-0079920.  
XX 30-MAR-1998; 98US-0079923.  
XX 31-MAR-1998; 98US-0080105.  
XX 31-MAR-1998; 98US-0080107.  
XX 31-MAR-1998; 98US-0080165.  
XX 31-MAR-1998; 98US-0080194.  
XX 01-APR-1998; 98US-0080327.  
XX 01-APR-1998; 98US-0080328.  
XX 01-APR-1998; 98US-0080333.  
XX 01-APR-1998; 98US-0080334.  
XX 08-APR-1998; 98US-0081049.  
XX 08-APR-1998; 98US-0081070.  
XX 08-APR-1998; 98US-0081071.  
XX 09-APR-1998; 98US-0081195.  
XX 09-APR-1998; 98US-0081203.  
XX 09-APR-1998; 98US-0081229.  
XX 15-APR-1998; 98US-0081817.  
XX 15-APR-1998; 98US-0081838.  
XX 15-APR-1998; 98US-0081952.  
XX 15-APR-1998; 98US-0081955.  
XX 21-APR-1998; 98US-0082568.  
XX 21-APR-1998; 98US-0082569.  
XX 22-APR-1998; 98US-0082700.  
XX 22-APR-1998; 98US-0082704.  
XX 23-APR-1998; 98US-0082804.  
XX 23-APR-1998; 98US-0082767.  
XX 23-APR-1998; 98US-0082796.  
XX 27-APR-1998; 98US-0083336.  
XX 28-APR-1998; 98US-0083322.  
XX 29-APR-1998; 98US-0083392.  
XX 29-APR-1998; 98US-0083495.  
XX 29-APR-1998; 98US-0083496.  
XX 29-APR-1998; 98US-0083499.  
XX 29-APR-1998; 98US-0083500.  
XX 29-APR-1998; 98US-0083545.  
XX 29-APR-1998; 98US-0083554.  
XX 29-APR-1998; 98US-0083558.  
XX 29-APR-1998; 98US-0083559.  
XX 30-APR-1998; 98US-0083742.







Db 1087 CCAATTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGTC 1146  
QY 784 TCCCAATTTGCAATGAATGTCATGTCCTCAAGCAAAAGTTACTAAAAAATACACGAGG 843  
Db 1147 TCCCAATTTGCAATGAATGTCATGTCCTCAAGCAAAAGTTACTAAAAAATACACGAGG 1206  
QY 844 TCCCTTCAGTTGAGACCAAAACCCGGTGTGAGGGATTGCACAAATCACTACCGACGTTGG 903  
Db 1207 TCCCTTCAGTTGAGACCAAAAGCCGGTGTGAGGGATTGCACAAATCACTACCGACGTTGG 1266  
QY 904 CCCTGGAGCACATGAGAGAGTGTGACTGTGTGTCAGAGGGAGCAGGAGGATAGCCGC 963  
Db 1267 CCCTGGAGCACATGAGAGAGTGTGACTGTGTGTCAGAGGGAGCAGGAGGATAGCCGC 1326  
QY 964 ATCCACACAGCAGCTCTTGGCCAGAGCTGTGTCAGTGCAGTGGCTGATTCATTAGAGAA 1023  
Db 1327 ATCCACACAGCAGCTCTTGGCCAGAGCTGTGTCAGTGCAGTGGCTGATTCATTAGAGAA 1386  
QY 1024 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTTGTCTTCAAGACCTTTTCATCTTCAG 1083  
Db 1387 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTTGTCTTCAAGACCTTTTCATCTTCAG 1446  
QY 1084 GATTTACAGTGCATTTCTAAGAGAGAGACATCACAAGAAATAGAGTTGTGCACAGCT 1143  
Db 1447 GATTTACAGTGCATTTCTAAGAGAGAGACATCACAAGAAATAGAGTTGTGCACAGCT 1506  
QY 1144 CTTTGTGAGAGGCGCTTAAAGACAGGAGAGAAAGCTCTTCAATCGTGAAGAAATTA 1203  
Db 1507 CTTTGTGAGAGGCGCTTAAAGACAGGAGAGAAAGCTCTTCAATCGTGAAGAAATTA 1566  
QY 1204 ATGTTGTTAAATAGATCACAGCTAGTTTCAGAGTTACCATGTAATTTCCACTAGC 1263  
Db 1567 ATGTTGTTAAATAGATCACAGCTAGTTTCAGAGTTACCATGTAATTTCCACTAGC 1626  
QY 1264 TGGGTTCTGTTATTTTCAGTTCTTTCGATACGCTTAGGTTAATGTCAGTACAGGAA 1323  
Db 1627 TGGGTTCTGTTATTTTCAGTTCTTTCGATACGCTTAGGTTAATGTCAGTACAGGAA 1686  
QY 1324 CTGTGCAAGTGAGCACCTGATTCGTTGCTTGTCTTAACTTAAAGCTCCATGTCCTGG 1383  
Db 1687 CTGTGCAAGTGAGCACCTGATTCGTTGCTTGTCTTAACTTAAAGCTCCATGTCCTGG 1746  
QY 1384 CCTAAATCGTATAAAATCTGATTTTCTTTTCTTTTCTTCTATATACATATGAA 1443  
Db 1747 CCTAAATCGTATAAAATCTGATTTTCTTTTCTTTTCTTCTATATACATATGAA 1806  
QY 1444 ACCAGACATCTATGTACTACAAACCTGGTTTAAAGAGAACTATGTTGCTATGAT 1503  
Db 1807 ACCAGACATCTATGTACTACAAACCTGGTTTAAAGAGAACTATGTTGCTATGAT 1866  
QY 1504 TAAACTTGTCTGATGATAGGACAGACTGGA 1536  
Db 1867 TAAACTTGTCTGATGATAGGACAGACTGGA 1899

RESULT 6  
AAA88515  
ID AAA88515 standard; cDNA; 2849 BP.

AC AAA88515;

DT 22-JAN-2001 (first entry)

XX Human PRO200 (VEGF-E) cDNA clone DNA29101-1272.

XX PRO200: vascular epithelial growth factor E; VEGF-E; human;  
KW ocular disease; retinopathy; maculopathy; therapy;  
KW retinitis pigmentosa; macular degeneration; retinal detachment;  
KW retinal tear; macular hole; myopia; traumatic choroidopathy;  
KW acute retinal necrosis syndrome; contusion; edema;  
KW retinal vision occlusion; vascular disease; retinal vasculitis;  
KW thrombocytopenic purpura; uveitis; retinal occlusion; ss.

XX OS Homo sapiens.  
XX PH Key Location/Qualifiers  
FT CDS 285..1322  
FT sig\_peptide /\*tag= a  
FT mat\_peptide /\*tag= b  
FT 327..1319  
XX /\*tag= c  
XX WO200053760-A2.  
XX 14-SEP-2000.  
XX 10-MAR-2000; 2000WO-US06319.  
XX 12-MAR-1999; 99US-0123957.  
XX (GETH ) GENENTECH INC.  
XX Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ, Kabakoff RC;  
XX Klein RD, Kijavini IJ, Kuo SS, La Fleur M, Wood WI;  
XX WPI; 2000-587437/55.  
XX P-PSDB; AAB19578.  
XX Novel PRO polypeptides useful for preventing or rescuing retinal cells  
XX from injury caused by ocular diseases such as retinitis pigmentosa,  
XX retinopathy, retinal degenerative diseases, degenerative myopia,  
XX uveitis -  
XX Example 8; Fig 1; 140pp; English.

XX The present sequence is that of cDNA clone DNA29101-1272 or UNQ174  
XX (ATCC 209553) isolated from a human glioma cell line G61 CDNA  
XX library using probes (see AAA8523-26) based on an expressed sequence  
XX tag (see AAA8523-26) identified on the basis of homology to vascular  
XX endothelial growth factor (VEGF). The clone contains a single open  
XX reading frame encoding a 345-amino acid protein (see AAB19578)  
XX designated PRO200 or VEGF-E. The isolated cDNA can be used in the  
XX recombinant production of PRO200 (VEGF-E). The invention relates  
XX to the use of PRO polypeptides, including PRO200, to delay, prevent  
XX or rescue retinal cells such as retinal neurons selected from  
XX photoreceptors, retinal ganglion cells, displaced retinal ganglion  
XX cells, amacrine cells, displaced amacrine cells, horizontal and  
XX bipolar neurons, and supportive cells (including Mueller cells and  
XX pigment epithelial cells) from injury and degradation. The retinal  
XX cells are preferably photoreceptors and photoreceptor cell injury or  
XX death is caused by retinal injury, light or environmental trauma or  
XX by an ocular disease selected from retinitis pigmentosa, macular  
XX degeneration, including age-related, retinal detachment, retinal  
XX tears, retinopathy, retinal degenerative diseases, macular holes,  
XX degenerative myopia, acute retinal necrosis syndrome, traumatic  
XX chorioretinopathies or contusion such as Purtscher's retinopathy,  
XX edema, ischemic conditions such as central or branch retinal vision  
XX occlusion, collagen vascular diseases, thrombocytopenic purpura,  
XX uveitis, retinal vasculitis and occlusion associated with Eales  
XX disease and systemic lupus erythematosus (claimed).

SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 99.8%; Score 1532.6; DB 21; Length 2849;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTAAATTCAGTTTCCAGCAACAGGAAACAGACGGAGTCAAGATCCTCAGCATGAGA 63  
Db 367 GTAAATTCAGTTTCCAGCAACAGGAAACAGACGGAGTCAAGATCCTCAGCATGAGA 426  
QY 64 GAATTTATTTACTGTCCTACTTAATGAGTATTTTCAGCCCAAGGTTTCTCATCTTATC 123  
Db 427 GAATTTATTTACTGTCCTACTTAATGAGTATTTTCAGCCCAAGGTTTCTCATCTTATC 486

```
QY 124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATACAAAC 183
Db 487 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATACAAAC 546
QY 184 TTACGTTTGATGAAGATTTCGGCTTGAAGCCAGAGATGACATATGCAAGTATGATT 243
Db 547 TTACGTTTGATGAAGATTTCGGCTTGAAGCCAGAGATGACATATGCAAGTATGATT 606
QY 244 TTGTAGAAAGTTGAGGAAACCCAGTGTATGAACTATATTAGGGCGCTGGTGTCTCGGTA 303
Db 607 TTGTAGAAAGTTGAGGAAACCCAGTGTATGAACTATATTAGGGCGCTGGTGTCTCGGTA 666
QY 304 CTGTACCAAGGAAAAAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 363
Db 667 CTGTACCAAGGAAAAAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 726
QY 364 AATATTTTCCCTTCGAACCAAGGTTCTGCATCCACTACAACTTCTCATGCGCAATTTCA 423
Db 727 AATATTTTCCCTTCGAACCAAGGTTCTGCATCCACTACAACTTCTCATGCGCAATTTCA 786
QY 424 CAGAAAGTGTGAGTCTCTTTCAGTGTACCCCTTTCAGCTTTGCACTGGACCTGCTTAATA 483
Db 787 CAGAAAGTGTGAGTCTCTTTCAGTGTACCCCTTTCAGCTTTGCACTGGACCTGCTTAATA 846
QY 484 ATGCTATAAATGCTCTTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 543
Db 847 ATGCTATAAATGCTCTTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 906
QY 544 GGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 603
Db 907 GGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 966
QY 604 TTTTGTGAAGAAATCCAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 663
Db 967 TTTTGTGAAGAAATCCAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1026
QY 664 ACAGTGCACACTGCTGTAATCTCAGTGTGCTCAATGAGGAGAACTAAAGAGAACCGATA 723
Db 1027 ACAGTGCACACTGCTGTAATCTCAGTGTGCTCAATGAGGAGAACTAAAGAGAACCGATA 1086
QY 724 CCATTTTCGCCAGGTTGCTCCTCGTTAAACGCTGTGGTGGAACTGCTCCTGTTGTC 783
Db 1087 CCATTTTCGCCAGGTTGCTCCTCGTTAAACGCTGTGGTGGAACTGCTCCTGTTGTC 1146
QY 784 TCCCAATTCGAATGAATGTCAATGTGTCCCAAGCAAAAGTTTACTAAAAAATACCAAGAGG 843
Db 1147 TCCCAATTCGAATGAATGTCAATGTGTCCCAAGCAAAAGTTTACTAAAAAATACCAAGAGG 1206
QY 844 TCCCTTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCGCAAAATCACTCCACGAGTGG 903
Db 1207 TCCCTTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCGCAAAATCACTCCACGAGTGG 1266
QY 904 CCCTTGAGACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGAGGATAGCCGC 963
Db 1267 CCCTTGAGACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGAGGATAGCCGC 1326
QY 964 ATCAACCAAGCAGCTCTTTCGCCAGAGCTGTGCAAGTGTGAGTGTGAGTGTGAGTGTGAGT 1023
Db 1327 ATCAACCAAGCAGCTCTTTCGCCAGAGCTGTGCAAGTGTGAGTGTGAGTGTGAGTGTGAGT 1386
QY 1024 CGTATGCGTTATCTCCATCCTTATCTCAGTGTGTTGTTTCAAGGACCTTTCATCTTCAG 1083
Db 1387 CGTATGCGTTATCTCCATCCTTATCTCAGTGTGTTTGTCTTCAAGGACCTTTCATCTTCAG 1446
QY 1084 GATTTCAGTGCATTTCTGAAAGAGAGACATCAAAACAGAAATTTAGGAGTTGTGCAACAGCT 1143
Db 1447 GATTTCAGTGCATTTCTGAAAGAGAGACATCAAAACAGAAATTTAGGAGTTGTGCAACAGCT 1506
QY 1144 CTTTGTGAGAGGCGCTTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTA 1203
Db 1507 CTTTGTGAGAGGCGCTTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTA 1566
```

RESULT 7  
AAC58579

ID AAC58579 standard; cDNA; 2849 BP.

AC AAC58579;

XX 29-JAN-2001 (first entry)

DE Human PRO200 protein UNQ174 encoding cDNA SEQ ID NO:1.

XX Human; immune related disease; diagnosis; Sjogren's syndrome; thyroiditis; cardiant;  
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
KW autoimmune thrombocytopenia; immune-mediated renal disease;  
KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW autoimmune disease; immune-mediated skin disease; allergic disease;  
KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease; ss.

XX Homo sapiens.

PN WO200053758-A2.

XX 14-SEP-2000.

XX 02-MAR-2000; 2000WO-US05841.

XX 08-MAR-1999; 99WO-US05028.

PR 10-MAR-1999; 99US-0123618.

PR 12-MAR-1999; 99US-0123957.

PR 23-MAR-1999; 99US-0125775.

PR 12-APR-1999; 99US-0128849.

PR 20-APR-1999; 99WO-US08615.

PR 28-APR-1999; 99US-0131445.

PR 04-MAY-1999; 99US-0132371.

PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US22089.  
PR 29-OCT-1999; 99US-0162506.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30999.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
XX  
XX WPI; 2000-572271/53.  
DR P-PSDB; AAB33414.  
XX  
XX sixty four PRO polypeptides, useful in the diagnosis and treatment of  
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
XX  
XX Claim 23; Fig 1; 309pp; English.  
XX  
XX The present invention describes sixty four human PRO proteins which can  
CC be used in the treatment of immune related diseases. The human PRO  
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
CC treating and diagnosing immune related disorders. The disorders are  
CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
CC autoimmune or immune-mediated skin diseases, allergic diseases,  
CC immunological diseases of the lung, and transplantation associated  
CC diseases including graft rejection and graft-versus-host-disease.  
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 99.8%; Score 1532.6; DB 21; Length 2849;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTPAATTCAGTTTCCGACACAGGACAGAACGGAGTACAGATCCTCAGCATGAGA 63  
DB |||||||  
DB 367 GTPAATTCAGTTTCCGACACAGGACAGAACGGAGTACAGATCCTCAGCATGAGA 426  
|||  
QY 64 GAAATTATTACTGTCTACTAATGGAAGTATTACAGGCCCAAGGTTTCTCTACTATTTC 123  
DB |||||||  
DB 427 GAAATTATTACTGTCTACTAATGGAAGTATTACAGGCCCAAGGTTTCTCTACTATTTC 486  
|||

QY 124 CAAGAAATACGGTCTTGGTATCGAGATTAGTAGCAGTAGAGAAATGTATGATCAAC 183  
|||  
DB 487 CAAGAAATACGGTCTTGGTATCGAGATTAGTAGCAGTAGAGAAATGTATGATCAAC 546  
|||  
QY 184 TTACGTTTGATCAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTAGTATT 243  
DB 547 TTACGTTTGATCAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTAGTATT 606  
|||  
QY 244 TTGTAGAGTTGAGGAACCCAGTGTGAACTATATTAGGGCGCTGGTCTCGGTA 303  
DB 607 TTGTAGAGTTGAGGAACCCAGTGTGAACTATATTAGGGCGCTGGTCTCGGTA 666  
|||  
QY 304 CTGTACCAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATG 363  
DB 667 CTGTACCAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATG 726  
|||  
QY 364 AATATTTTCCTTCTGAACACAGGGTCTGCATCCATCAACATTTGTCATGCCACAATTCA 423  
DB 727 AATATTTTCCTTCTGAACACAGGGTCTGCATCCATCAACATTTGTCATGCCACAATTCA 786  
|||  
QY 424 CAGAAGCTGTGAGTCTTTCAGTGTACCCCTTTCAGCTTTGCCACTTGGACCTGCTTAATA 483  
DB 787 CAGAAGCTGTGAGTCTTTCAGTGTACCCCTTTCAGCTTTGCCACTTGGACCTGCTTAATA 846  
|||  
QY 484 ATGCTATAACCTGCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACACAGAGAT 543  
DB 847 ATGCTATAACCTGCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACACAGAGAT 906  
|||  
QY 544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 603  
DB 907 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 966  
|||  
QY 604 TTTTGGAGAAATCCAGAGTGTGATCTCAACCTTCTTAACAGAGGAGTAAAGATTAT 663  
DB 967 TTTTGGAGAAATCCAGAGTGTGATCTCAACCTTCTTAACAGAGGAGTAAAGATTAT 1026  
|||  
QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 723  
DB 1027 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 1086  
|||  
QY 724 CCAATTTCTGGCCAGGTTGTCTCTCGTTAAACGCTGTGTGGGAACTGTGCTGTGTC 783  
DB 1087 CCAATTTCTGGCCAGGTTGTCTCTCGTTAAACGCTGTGTGGGAACTGTGCTGTGTC 1146  
|||  
QY 784 TCCACAAATTGCAATCAATGTCAATGTCTCCCAAGCAAGCTTACTAAAAATACCAAGG 843  
DB 1147 TCCACAAATTGCAATCAATGTCAATGTCTCCCAAGCAAGCTTACTAAAAATACCAAGG 1206  
|||  
QY 844 TCCTTCAGTTGAGACCAASACCGGTGTCCAGGGATTGCACAAATCACTCACCGAGTGG 903  
DB 1207 TCCTTCAGTTGAGACCAASACCGGTGTCCAGGGATTGCACAAATCACTCACCGAGTGG 1266  
|||  
QY 904 CCCTGAGACCATGACAGAGTGTGATGTGTGACAGAGGAGCAGCAGAGATAGCCGC 963  
DB 1267 CCCTGAGACCATGACAGAGTGTGATGTGTGACAGAGGAGCAGCAGAGATAGCCGC 1326  
|||  
QY 964 ATCACACACAGCAGCTCTTGGCCAGAGCTGTGACGTGACGTGGCTGATTTCTATTAGAGAA 1023  
DB 1327 ATCACACACAGCAGCTCTTGGCCAGAGCTGTGACGTGACGTGGCTGATTTCTATTAGAGAA 1386  
|||  
QY 1024 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTGCTTCAAGGACCTTTTCATCTTCAG 1083  
DB 1387 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTGCTTCAAGGACCTTTTCATCTTCAG 1446  
|||  
QY 1084 GATTACAGTGCATCTGAAAGAGAGACATCAAAAGATTTAGAGTTGTGCAACAGCT 1143  
DB 1447 GATTACAGTGCATCTGAAAGAGAGACATCAAAAGATTTAGAGTTGTGCAACAGCT 1506  
|||  
QY 1144 CTTTGGAGAGGCGCTAAAGACAGGAGAAAGGTCTTCAATCGTGAAGAAATTA 1203  
DB 1507 CTTTGGAGAGGCGCTAAAGACAGGAGAAAGGTCTTCAATCGTGAAGAAATTA 1566  
|||



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QY 664 ACAGTCGCACACCTCGTAACCTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCCGATA 723
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1027 ACAGTCGCACACCTCGTAACCTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCCGATA 1086
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 724 CCATTTTCTGGCCAGGTTGCTCTCTGTTAAACGCTGTGTGGAACTGTGCGCTTGTGTC 783
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1087 CCATTTTCTGGCCAGGTTGCTCTCTGTTAAACGCTGTGTGGAACTGTGCGCTTGTGTC 1146
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 784 TCCCAATTCGAATGATCAATGTGTCCCAAGCAAAAGTTACTAAAARATACCAACGAGG 843
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1147 TCCCAATTCGAATGATCAATGTGTCCCAAGCAAAAGTTACTAAAARATACCAACGAGG 1206
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 844 TCCCTTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCACAAATCACTACCCAGCCTGG 903
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1207 TCCCTTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCACAAATCACTACCCAGCCTGG 1266
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 904 CCCTGGAGCACCATGAGAGGTGACTGTGTGTCAGAGGGAGCAGAGGATAGCCGC 963
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1267 CCCTGGAGCACCATGAGAGGTGACTGTGTGTCAGAGGGAGCAGAGGATAGCCGC 1326
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 964 ATCAACACAGCAGCTCTTGCCACAGAGCTGTGCAGTGCAGTGGCTGATTCATTATAGAGAA 1023
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1327 ATCAACACAGCAGCTCTTGCCACAGAGCTGTGCAGTGCAGTGGCTGATTCATTATAGAGAA 1386
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1024 CGTATGCGTTATCTCCATCTCTTAATCTCAGTTGTTGCTTCAAGGACCTTTTCATCTTCAG 1083
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1387 CGTATGCGTTATCTCCATCTCTTAATCTCAGTTGTTGCTTCAAGGACCTTTTCATCTTCAG 1446
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1084 GATTTACAGTCATCTGAAAGAGAGACATCAACACAGAAATAGAGTTGTGCAACAGCT 1143
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1447 GATTTACAGTCATCTGAAAGAGAGACATCAACACAGAAATAGAGTTGTGCAACAGCT 1506
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1144 CTTTTGAGAGAGGCGCTTAAAGACAGGAGAAAGGTCTTCAATCGTGAAGAAATTA 1203
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1507 CTTTTGAGAGAGGCGCTTAAAGACAGGAGAAAGGTCTTCAATCGTGAAGAAATTA 1566
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1204 ATGTTGTATTAATAGATACACAGCTAGTTTCAGAGTTACCATGTAGTATTCACATAGC 1263
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1567 ATGTTGTATTAATAGATACACAGCTAGTTTCAGAGTTACCATGTAGTATTCACATAGC 1626
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1264 TGGGTTCTGTATTTTCAGTTCTTTTCGATACGCTTAGGTATGTACGTACAGGAAAAA 1323
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1627 TGGGTTCTGTATTTTCAGTTCTTTTCGATACGCTTAGGTATGTACGTACAGGAAAAA 1686
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1324 CTGTGCAAGTGAGACACCTGATTCGCTTGCCTTGAATCTAAAGCTCCCATGTCCTGGG 1383
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1687 CTGTGCAAGTGAGACACCTGATTCGCTTGCCTTGAATCTAAAGCTCCCATGTCCTGGG 1746
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1384 CCTAAATCGTATTAATAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTA 1443
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1747 CCTAAATCGTATTAATAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTA 1806
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1444 ACCAGACATTTCTATGTACTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATGTAAT 1503
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1807 ACCAGACATTTCTATGTACTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATGTAAT 1866
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1504 TAAACTTGTGTCACTGCTGATAGGACAGACTGGA 1536
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1867 TAAACTTGTGTCACTGCTGATAGGACAGACTGGA 1899
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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## RESULT 9

AAS21386

ID AAS21386 standard; cDNA; 2849 BP.

XX AC AAS21386;

XX AC AAS21386;

DT 24-OCT-2001 (first entry)

XX Human cDNA sequence encoding for PRO200 polypeptide.

DE Human secretory and transmembrane; PRO; mammalian; cancer; lung;

KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;

breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.

Homo sapiens.

W0200140466-A2.

07-JUN-2001.

01-DEC-2000; 2000WO-US32678.

01-DEC-1999; 99WO-US28301.

01-DEC-1999; 99WO-US28634.

02-DEC-1999; 99WO-US28551.

02-DEC-1999; 99WO-US28564.

02-DEC-1999; 99WO-US28565.

09-DEC-1999; 99US-0170262.

16-DEC-1999; 99WO-US30095.

20-DEC-1999; 99WO-US30911.

20-DEC-1999; 99WO-US30999.

30-DEC-1999; 99WO-US31243.

06-JAN-2000; 2000WO-US00277.

06-JAN-2000; 2000WO-US00376.

11-FEB-2000; 2000WO-US03565.

18-FEB-2000; 2000WO-US04341.

18-FEB-2000; 2000WO-US04342.

22-FEB-2000; 2000WO-US04414.

24-FEB-2000; 2000WO-US04914.

24-FEB-2000; 2000WO-US05004.

01-MAR-2000; 2000WO-US05601.

21-MAR-2000; 2000WO-US07377.

30-MAR-2000; 2000WO-US07532.

17-MAY-2000; 2000WO-US08439.

22-MAY-2000; 2000WO-US13705.

30-MAY-2000; 2000WO-US14042.

02-JUN-2000; 2000WO-US14941.

10-NOV-2000; 2000WO-US15264.

10-NOV-2000; 2000WO-US30873.

(GETH ) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;

Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-408281/43.

P-FSDB; AAU12314.

Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical -

Claim 3; Fig 285; 813pp; English.

AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify

CC molecules involved in binding interactions. The polynucleotides encoding  
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
CC transgenic or knock out animals and can be used in gene therapy.  
XX  
SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 99.8%; Score 1532.6; DB 22; Length 2849;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	4	GTAATTCAGTTTCCAGCAACAGGAGTACAGAGTCAAGATCTCTCAGCATGAGA	63
Db	367	GTAATTCAGTTTCCAGCAACAGGAGTACAGAGTCAAGATCTCTCAGCATGAGA	426
QY	64	GAATTTACTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCATCTTATC	123
Db	427	GAATTTACTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCATCTTATC	486
QY	124	CAAGAAATACGGTCTTGGTATGAGATTAGTAGCAGTAGAGGAAATGTATGGATCAAC	183
Db	487	CAAGAAATACGGTCTTGGTATGAGATTAGTAGCAGTAGAGGAAATGTATGGATCAAC	546
QY	184	TTACGTTTGGATGAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT	243
Db	547	TTACGTTTGGATGAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT	506
QY	244	TGTTAGAGTTGAGAAACCAAGTATGGAACATATATTAGGCGCTGGTGTCTCGGTA	303
Db	607	TGTTAGAGTTGAGAAACCAAGTATGGAACATATATTAGGCGCTGGTGTCTCGGTA	666
QY	304	CTGTACACAGGAAACAGAGTTTCTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATG	363
Db	667	CTGTACACAGGAAACAGAGTTTCTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATG	726
QY	364	AATATTTTCTTCTGAACACAGGTTCTGCATCCACTACAAATTTGTCATGCCAATTCAC	423
Db	727	AATATTTTCTTCTGAACACAGGTTCTGCATCCACTACAAATTTGTCATGCCAATTCAC	786
QY	424	CAGAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTCAGCTGACCTGCTTAATA	483
Db	787	CAGAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTCAGCTGACCTGCTTAATA	846
QY	484	ATGCTATAATGCTCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTGAACACAGAGAT	543
Db	847	ATGCTATAATGCTCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTGAACACAGAGAT	906
QY	544	GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG	603
Db	907	GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG	966
QY	604	TTTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTACAGAGAGGTAAAGATTAT	663
Db	967	TTTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTACAGAGAGGTAAAGATTAT	1026
QY	664	ACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA	723
Db	1027	ACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA	1086
QY	724	CAATTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGTGGGAACCTGTGCTGTGTC	783
Db	1087	CAATTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGTGGGAACCTGTGCTGTGTC	1146
QY	784	TCCCAATTTGCAATGAATGCAATGTCTTCCAGCAAAAGTTACTAAAAATACCAAGAGG	843
Db	1147	TCCCAATTTGCAATGAATGCAATGTCTTCCAGCAAAAGTTACTAAAAATACCAAGAGG	1206
QY	844	TCCTTCAGTTGAGACAAASACCGGTGTGAGGGGATTCACAAATCACTCACCGACGTGG	903
Db	1207	TCCTTCAGTTGAGACAAASACCGGTGTGAGGGGATTCACAAATCACTCACCGACGTGG	1266
QY	904	CCCTGGAGCAACATGAGAGTGTGATCTGTGTGTGAGAGGGAGCACAGGAGGATACCGCC	963
Db	1267	CCCTGGAGCAACATGAGAGTGTGATCTGTGTGTGAGAGGGAGCACAGGAGGATACCGCC	1326

QY	964	ATCACACACAGCAGCTCTTGGCCACAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAA	1023
Db	1327	ATCACACACAGCAGCTCTTGGCCACAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAA	1386
QY	1024	CGTATCGGTATCTCCATCCCTTAATCTCAGTTGTTTGGCTTCAAGACCTTTCATCTTCAG	1083
Db	1387	CGTATCGGTATCTCCATCCCTTAATCTCAGTTGTTTGGCTTCAAGACCTTTCATCTTCAG	1446
QY	1084	GAATTTACAGTGCATTTCTGAAGAGGAGACATCAACACAGAAATTAGGAGTTGTGCAACAGCT	1143
Db	1447	GAATTTACAGTGCATTTCTGAAGAGGAGACATCAACACAGAAATTAGGAGTTGTGCAACAGCT	1506
QY	1144	CTTTTGAAGAGGCGCTAAAGACAGGAGAAAAGTCTTCAATCTGTGGAAGAAAATTAA	1203
Db	1507	CTTTTGAAGAGGCGCTAAAGACAGGAGAAAAGTCTTCAATCTGTGGAAGAAAATTAA	1566
QY	1204	ATGTTGTATTAATAGATCACCAGCTAGTTTTCAGAGTTTACCATTGTTACCTATTCCTAGC	1263
Db	1567	ATGTTGTATTAATAGATCACCAGCTAGTTTTCAGAGTTTACCATTGTTACCTATTCCTAGC	1626
QY	1264	TGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTCAGTACAGGAAAAAA	1323
Db	1627	TGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTCAGTACAGGAAAAAA	1686
QY	1324	CTGTGCAATGTAGCACCCTGATTCCTGTTGCTTCTTAACCTTAAAGCTCCATGTCTCTGGG	1383
Db	1687	CTGTGCAATGTAGCACCCTGATTCCTGTTGCTTCTTAACCTTAAAGCTCCATGTCTCTGGG	1746
QY	1384	CCTAAATTCGTATAAATCTGGAATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTA	1443
Db	1747	CCTAAATTCGTATAAATCTGGAATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTA	1806
QY	1444	ACCAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT	1503
Db	1807	ACCAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT	1866
QY	1504	TAAACTTGTGTCTGCTGATAGGACAGACTGGA	1536
Db	1867	TAAACTTGTGTCTGCTGATAGGACAGACTGGA	1899
RESULT 10			
AAC90564			
ID	AAC90564 standard; cDNA; 2849 BP.		
XX	AC AAC90564;		
XX	AC AAC90564;		
DT	21-MAR-2001 (first entry)		
XX	Human PRO200 cDNA.		
DE	Human; PRO; cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;		
KW	vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;		
KW	vulnerable; antianginal; gene therapy; cardiovascular disease;		
KW	endothelial disorder; angiogenic disorder; cancer; periodontal disease;		
KW	wound healing; ss.		
OS	Homo sapiens.		
XX	WO200073445-A2.		
FN	07-DEC-2000.		
PD	17-MAY-2000; 2000WO-US13705.		
PF	02-JUN-1999; 99WO-US12252.		
XX	23-JUN-1999; 99US-0141037.		
PR	20-JUL-1999; 99US-0144758.		
PR	26-JUL-1999; 99US-0145698.		
PR	28-JUL-1999; 99US-0146222.		
PR	01-SEP-1999; 99WO-US20111.		
PR	30-NOV-1999; 99WO-US28313.		

PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WJ;  
XX  
DR WPI; 2001-025251/03.  
DR P-PSDB; AAB50952.  
XX  
XX Seventeen nucleic acids encoding PRO polypeptides which are useful in  
PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
PT disorders in a mammal -  
XX  
PS Claim 60; Fig 3; 182pp; English.  
XX  
CC The present sequence is one of seventeen nucleic acids encoding PRO  
CC polypeptides. The PRO nucleic acids, polypeptides, agonists and  
CC antagonists are useful for treating cardiovascular, endothelial or  
CC angiogenic disorders in a mammal. Examples of these disorders include  
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, Reynaud's disease,  
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis  
CC and lymphangitis. The PRO polypeptides and antagonists are also used to  
CC prevent tumour angiogenesis and for treating periodontal diseases. They  
CC are also used to stimulate wound healing and tissue regeneration.  
CC The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful  
CC for diagnosing a cardiovascular, endothelial or angiogenic disorder.  
XX  
SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;  
  
Query Match 99.8%; Score 1532.6; DB 22; Length 2849;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 GTAAATTCAGTTTCCAGCAACAGGACAGACGGAGTACAGATCCTCAGCATGAGA 63  
DB 367 GTAAATTCAGTTTCCAGCAACAGGACAGACGGAGTACAGATCCTCAGCATGAGA 426  
  
QY 64 GAAATTTACTGTGTCTACTAATGGAAGTATTACAGGCCCAAGGTTTCTCTACTATTATC 123  
DB 427 GAAATTTACTGTGTCTACTAATGGAAGTATTACAGGCCCAAGGTTTCTCTACTATTATC 486  
  
QY 124 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGATGATACAAAC 183  
DB 487 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGATGATACAAAC 546  
  
QY 184 TTACGTTTGTATGAAGATTTGGCTTTGAAGACCCAGAGTACATATGCAAGTATGATT 243  
DB 547 TTACGTTTGTATGAAGATTTGGCTTTGAAGACCCAGAGTACATATGCAAGTATGATT 606  
  
QY 244 TTGTAGAAGTTGAGGAACCCAGTGTAGTGAATATATTAGGGCGCTGGTGTCTCTGGTA 303  
DB 607 TTGTAGAAGTTGAGGAACCCAGTGTAGTGAATATATTAGGGCGCTGGTGTCTCTGGTA 666  
  
QY 304 CTGTACCAAGAAACAGATTTCTAAAGGAAATCAATTAGGATAAGATTTGATCTGATG 363  
DB 667 CTGTACCAAGAAACAGATTTCTAAAGGAAATCAATTAGGATAAGATTTGATCTGATG 726  
  
QY 364 AATATTTCTCTGACACAGGTTCTGCATCCACTACACATTTGTCAGCCACATTTCA 423  
DB

DB 727 AATATTTCTCTGACACAGGGTTCTGCATCCATCAACAATTTGTCTATGCCACAATTCA 786  
QY 424 CAGAGCTGTGAGTCTCTTTCAGTGTCTACCCCTTTCAGCTTTGCTGACCTGCTCTAATA 483  
DB 787 CAGAAAGCTGTGAGTCTCTTTCAGTGTCTACCCCTTTCAGCTTTGCTGACCTGCTCTAATA 846  
QY 484 ATGCTATAAATCGCTTTAGTACCTTTGGAAGACCTTTATTTCGATATCTTGAACCAAGAGAT 543  
DB 847 ATGCTATAAATCGCTTTAGTACCTTTGGAAGACCTTTATTTCGATATCTTGAACCAAGAGAT 906  
QY 544 GGCAGTTGCACTTAGAAGATCTATATAGCCCAACTTGGCAACTCTTGGCAAGGCTTTTG 603  
DB 907 GGCAGTTGCACTTAGAAGATCTATATAGCCCAACTTGGCAACTCTTGGCAAGGCTTTTG 966  
QY 604 TTTTGGGAAGAAATCCAGAGTGTGGATCTGAACCTTCTAAACAGAGGAGTGAAGATTAT 663  
DB 967 TTTTGGGAAGAAATCCAGAGTGTGGATCTGAACCTTCTAAACAGAGGAGTGAAGATTAT 1026  
QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 723  
DB 1027 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 1086  
QY 724 CCAATTTCTGGCCAGGTTGTCTCTCTGTTAAACGCTGTGGTGGAACTGTGCTGTCTGTC 783  
DB 1087 CCAATTTCTGGCCAGGTTGTCTCTCTGTTAAACGCTGTGGTGGAACTGTGCTGTCTGTC 1146  
QY 784 TCCACAATTTGCAATGAATGTCAATGTGCCCAAGCAAGTCTTAAAAAATACCAGAGG 843  
DB 1147 TCCACAATTTGCAATGAATGTCAATGTGCCCAAGCAAGTCTTAAAAAATACCAGAGG 1206  
QY 844 TCCTTCAGTTGAGACCAAAACCCGTTGTCAGGGGATTCACAAATCACTCACCGACGTGG 903  
DB 1207 TCCTTCAGTTGAGACCAAAACCCGTTGTCAGGGGATTCACAAATCACTCACCGACGTGG 1266  
QY 904 CCCTCGAGCACCATCAGGAGTGTGATGTGTGTCAGAGGGAGCACAGAGGATACCCGC 963  
DB 1267 CCCTCGAGCACCATCAGGAGTGTGATGTGTGTCAGAGGGAGCACAGAGGATACCCGC 1326  
QY 964 ATCACACACAGCAGCTCTTGGCCAGAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAA 1023  
DB 1327 ATCACACACAGCAGCTCTTGGCCAGAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAA 1386  
QY 1024 CGTATGCGTTATCTCCATCCTTAAATCTCAGTTGTTTGTCTTCAAGGACCTTTCACTTCAG 1083  
DB 1387 CGTATGCGTTATCTCCATCCTTAAATCTCAGTTGTTTGTCTTCAAGGACCTTTCACTTCAG 1446  
QY 1084 GATTTACAGTGCATTTCTGAAAGAGAGACATCAACAGAAATTAGGAGTTGTCACAGCT 1143  
DB 1447 GATTTACAGTGCATTTCTGAAAGAGAGACATCAACAGAAATTAGGAGTTGTCACAGCT 1506  
QY 1144 CTTTTCAGAGGAGGCTTAAAGCACAGGAGAAAGGTCTTCAATCTGGAAGAGAAATTA 1203  
DB 1507 CTTTTCAGAGGAGGCTTAAAGCACAGGAGAAAGGTCTTCAATCTGGAAGAGAAATTA 1566  
QY 1204 ATGTTGTATTAATAGATCACAGCTAGTTTCAGAGTTTACCATGTCATGATTCCTACAGC 1263  
DB 1567 ATGTTGTATTAATAGATCACAGCTAGTTTCAGAGTTTACCATGTCATGATTCCTACAGC 1626  
QY 1264 TGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAA 1323  
DB 1627 TGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAA 1686  
QY 1324 CTGTGCAAGTACAGCACCTGATTCCCTTTCCTTTCCTTAACTTAAAGCTCCATGTCCTGGG 1383  
DB 1687 CTGTGCAAGTACAGCACCTGATTCCCTTTCCTTTCCTTTCCTTAAAGCTCCATGTCCTGGG 1746  
QY 1384 CTTAAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCAATATGATA 1443  
DB 1747 CTTAAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTACATATGATA 1806  
QY 1444 ACCAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAGAGAACTATGTTCTCTATGAT 1503  
DB 1807 ACCAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAGAGAACTATGTTCTCTATGAT 1866







Db 787 CAGAGCTGTGAGTCTCTCAGTGTACCCCTTTCAGCTTGGCACTGGACCTGCTTAATA 846  
QY 484 ATGCTATAAATCGCTTTAGTACTTGGAGACCTTATTCGATATCTTGAACAGAGAT 543  
Db 847 ATGCTATAAATCGCTTTAGTACTTGGAGACCTTATTCGATATCTTGAACAGAGAT 906  
QY 544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 603  
Db 907 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 966  
QY 604 TTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAATAT 663  
Db 967 TTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAATAT 1026  
QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGGAAGAACTTAAAGAGAACCGATA 723  
Db 1027 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGGAAGAACTTAAAGAGAACCGATA 1086  
QY 724 CCATTTTCTGGCCAGGTTGTCTCTGGTTAAACCGCTGTGGTGGAACTGTGCTGTGTC 783  
Db 1087 CCATTTTCTGGCCAGGTTGTCTCTGGTTAAACCGCTGTGGTGGAACTGTGCTGTGTC 1146  
QY 784 TCCACAATTCGAATGTCAATGTGTCCAGCAAGTACTTAAATAATACCAAGAGG 843  
Db 1147 TCCACAATTCGAATGTCAATGTGTCCAGCAAGTACTTAAATAATACCAAGAGG 1206  
QY 844 TCCTTCAGTTGAGACCAAAACCCGGTGTCCAGGGGATTCACAAATCACTCACCGACGTGG 903  
Db 1207 TCCTTCAGTTGAGACCAAAACCCGGTGTCCAGGGGATTCACAAATCACTCACCGACGTGG 1266  
QY 904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGTATGCCGC 963  
Db 1267 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGTATGCCGC 1326  
QY 964 ATCACCACAGCAGCTCTTGGCCAGAGCTGTGCAGTGCAGTGGCTGATCTATTAGAGAA 1023  
Db 1327 ATCACCACAGCAGCTCTTGGCCAGAGCTGTGCAGTGCAGTGGCTGATCTATTAGAGAA 1386  
QY 1024 CGTATGCTTATCTCCATCTTAAATCTCAGTTGTTTGTCTCAAGGACCTTTCATCTTCAAG 1083  
Db 1387 CGTATGCTTATCTCCATCTTAAATCTCAGTTGTTTGTCTCAAGGACCTTTCATCTTCAAG 1446  
QY 1084 GATTACAGTGCATTCTGAAGAGAGACATCAAAACAGAAATPAGAGTTGTGCACAGCT 1143  
Db 1447 GATTACAGTGCATTCTGAAGAGAGACATCAAAACAGAAATPAGAGTTGTGCACAGCT 1506  
QY 1144 CTTTGTGAGAGGGCTTAAAGACAGGAGAAAGTCTTCAATCGTGGAAAGAAATTA 1203  
Db 1507 CTTTGTGAGAGGGCTTAAAGACAGGAGAAAGTCTTCAATCGTGGAAAGAAATTA 1566  
QY 1204 ATGTTGTATTAATAGATCACAGCTAGTTTTCAGAGTTACCATGTACGTATTCCTAGC 1263  
Db 1567 ATGTTGTATTAATAGATCACAGCTAGTTTTCAGAGTTACCATGTACGTATTCCTAGC 1626  
QY 1264 TGGTTTCTGATTTTCAGTTCTTTTCATAGCGGTTAGGTTAATGTCACTACAGGAAAAA 1323  
Db 1627 TGGTTTCTGATTTTCAGTTCTTTTCATAGCGGTTAGGTTAATGTCACTACAGGAAAAA 1686  
QY 1324 CTGTGCAAGTGCACACCTGATTCCTGCTTTCATCTTAAAGTCCATGTCTGGG 1383  
Db 1687 CTGTGCAAGTGCACACCTGATTCCTGCTTTCATCTTAAAGTCCATGTCTGGG 1746  
QY 1384 CCTAAATCGTATAAATCTGGAATTTTTTTTTTTTTTGTCTCATATTCATATGTAA 1443  
Db 1747 CCTAAATCGTATAAATCTGGAATTTTTTTTTTTTTTGTCTCATATTCATATGTAA 1806  
QY 1444 ACCAGAACTTCTATGTACTACAAACCTGGTTTTTAAAGAACTATGTTGCTATGAAT 1503  
Db 1807 ACCAGAACTTCTATGTACTACAAACCTGGTTTTTAAAGAACTATGTTGCTATGAAT 1866  
QY 1504 TAACTTCGTATCCTGATAGGACAGACTGGA 1536

Db 1867 TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1899  
RESULT 13  
ID ACA03745 standard; cDNA; 2849 BP.  
AC ACA03745;  
XX  
DT 23-MAY-2003 (first entry)  
XX  
DE cDNA encoding human PRO polypeptide #143.  
XX  
KW Human; PRO polypeptide; secreted and transmembrane protein;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
KW differentiation; chondrocyte; tumour; genetic disorder;  
KW cytostatic; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2003036180-A1.  
XX  
PD 20-FEB-2003.  
XX  
PF 09-MAY-2002; 2002US-0143114.  
XX  
PR 31-MAR-1997; 97WO-US05230.  
PR 12-JUN-1998; 98WO-US12456.  
PR 14-JUL-1998; 98WO-US14552.  
PR 28-AUG-1998; 98WO-US17888.  
PR 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19093.  
PR 14-SEP-1998; 98WO-US19094.  
PR 14-SEP-1998; 98WO-US19177.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 29-OCT-1998; 98WO-US22991.  
PR 29-OCT-1998; 98WO-US22992.  
PR 20-NOV-1998; 98WO-US24855.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 10-MAR-1999; 99WO-US05190.  
PR 20-APR-1999; 99WO-US08615.  
PR 14-MAY-1999; 99WO-US10733.  
PR 02-JUN-1999; 99WO-US12252.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 22-DEC-1999; 99WO-US30999.  
PR 22-DEC-1999; 99WO-US30720.  
PR 30-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05746.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 22-JUN-2001; 2001WO-US20116.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 18-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 05-JUN-2001; 2001US-0874503.  
 PR 14-JUN-2001; 2001US-0882636.  
 PR 19-JUN-2001; 2001US-0886342.  
 PR 21-JUN-2001; 2001US-0887879.  
 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.

(GETH) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff B, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2003-332040/31.  
 DR P-PSDB; AB066712.

XX New secreted and transmembrane PRO nucleic acids, useful for gene  
 PT therapy, in chromosome and gene mapping, as chromosome markers, in  
 PT tissue typing, and in chromosome identification -

XX Claim 2; Fig 285; 660pp; English.

XX The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The  
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for  
 CC linking bioactive molecules to cells expressing PRO polypeptides,

CC for modulating biological activities of cells expressing PRO  
 CC polypeptides, and for identifying agonists or antagonists.  
 CC The PRO polypeptides are useful for stimulating the release of  
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating  
 CC the proliferation or differentiation of chondrocytes, and detecting the  
 CC presence of tumours. The polynucleotide sequences encoding PRO  
 CC polypeptides are useful as hybridisation probes, in chromosome and  
 CC gene mapping, in the generation of antisense RNA and DNA, in the  
 CC preparation of PRO polypeptides, for generating transgenic animals or  
 CC knockout animals, for the genetic analysis of individuals with genetic  
 CC disorders, and in gene therapy. ACA03603-ACA03877 represent CDNA  
 CC encoding the human PRO polypeptides of the invention.  
 CC Note: The sequence data for this patent was obtained in electronic  
 CC format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipsIDEntry.html.

XX Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 99.8%; Score 1532.6; DB 25; Length 2849;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTAAATCCAGTTTCCAGCAACAGGACAGAAACGAGTCAAGATCCTCAGCATGAGA 63  
 DB 367 GTAAATCCAGTTTCCAGCAACAGGACAGAAACGAGTCAAGATCCTCAGCATGAGA 426  
 QY 64 GAATTTATTACTGTGTCTACTAATGAAGTATTACAGCCCAAGGTTTCTCTACTATTATC 123  
 DB 427 GAATTTATTACTGTGTCTACTAATGAAGTATTACAGCCCAAGGTTTCTCTACTATTATC 486  
 QY 124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGAAATGTATGGATACAAC 183  
 DB 487 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGAAATGTATGGATACAAC 546  
 QY 184 TTACGTTTGTAGAAAGATTTCGGCTTGAAGACCCAGAGATGACATATGCAAGTAGTATT 243  
 DB 547 TTACGTTTGTAGAAAGATTTCGGCTTGAAGACCCAGAGATGACATATGCAAGTAGTATT 606  
 QY 244 TTGTAGAAAGTTGAGGAACCCAGTGTATGAACTATATTAGGGCGCTGGTGTCTCGTGA 303  
 DB 607 TTGTAGAAAGTTGAGGAACCCAGTGTATGAACTATATTAGGGCGCTGGTGTCTCGTGA 666  
 QY 304 CTGTACCAAGGAAAACAGATTTCCTAAAGGAAATCAAATTAGGATAGATTGTATCTGATG 363  
 DB 667 CTGTACCAAGGAAAACAGATTTCCTAAAGGAAATCAAATTAGGATAGATTGTATCTGATG 726  
 QY 364 AATATTTTCTCTGCAACAGGGTCTGCATCCACTACAACTTGTTCATGCCACAATTCA 423  
 DB 727 AATATTTTCTCTGCAACAGGGTCTGCATCCACTACAACTTGTTCATGCCACAATTCA 786  
 QY 424 CAGAAAGCTGTGAGTCTCTTCAGTGTACCCCTTCAGCTTTGCACTGGACCTGCTTAATA 483  
 DB 787 CAGAAAGCTGTGAGTCTCTTCAGTGTACCCCTTCAGCTTTGCACTGGACCTGCTTAATA 846  
 QY 484 ATGCTATAATCGCTTTTAGTACCTTGGAGACCTTATTTCGATATCTTGAACACAGAGAT 543  
 DB 847 ATGCTATAATCGCTTTTAGTACCTTGGAGACCTTATTTCGATATCTTGAACACAGAGAT 906  
 QY 544 GGCAGTTGGACTTAGAAGATCTATATAGCCCAACTTGGCAACTCTTGGCAAGGGCTTTTG 603  
 DB 907 GGCAGTTGGACTTAGAAGATCTATATAGCCCAACTTGGCAACTCTTGGCAAGGGCTTTTG 966  
 QY 604 TTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAAGATTAT 663  
 DB 967 TTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAAGATTAT 1026  
 QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGAGAACTAAAGAACCGATA 723  
 DB 1027 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGAGAACTAAAGAACCGATA 1086  
 QY 724 CCATTTTCTGCGCAGGTGTCTCCTGGTTAAACCGTGTGGGGAACTGTGCTGTGTC 783  
 DB 1087 CCATTTTCTGCGCAGGTGTCTCCTGGTTAAACCGTGTGGGGAACTGTGCTGTGTC 1146

QY 784 TCCACAAATGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTTACAAAAATACCAACGAGG 843  
Db 1147 TCCACAAATGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTTACAAAAATACCAACGAGG 1206  
QY 844 TCCTTCAGTTGAGACCAAAASACCGGTGTGCGGGGATTCGCAAAATCACTACCGACGTGG 903  
Db 1207 TCCTTCAGTTGAGACCAAAAGCCGGTGTGCGGGGATTCGCAAAATCACTACCGACGTGG 1266  
QY 904 CCCTGGAGACCAATGAGAGGTGCTACTGTGTGTCAGAGGGAGCACAGGAGATAGCCGC 963  
Db 1267 CCCTGGAGACCAATGAGAGGTGCTACTGTGTGTCAGAGGGAGCACAGGAGATAGCCGC 1326  
QY 964 ATCAACCAACGACGCTCTTTCGCCAGAGCTGTGCGAGTGCAGTGGCTGATTTCTATTAGAGAA 1023  
Db 1327 ATCAACCAACGACGCTCTTTCGCCAGAGCTGTGCGAGTGCAGTGGCTGATTTCTATTAGAGAA 1386  
QY 1024 CGTATCGTTATCTCCATCTTCTTAATCTCAGTGTGTTGCTTCAAGACCTTTCATCTTCAG 1083  
Db 1387 CGTATCGTTATCTCCATCTTCTTAATCTCAGTGTGTTGCTTCAAGACCTTTCATCTTCAG 1446  
QY 1084 GATTTACAGTGCATCTCTGAAAGAGAGACATCAACACAGAAATTAGAGTGTGCAACAGCT 1143  
Db 1447 GATTTACAGTGCATCTCTGAAAGAGAGACATCAACACAGAAATTAGAGTGTGCAACAGCT 1506  
QY 1144 CTTTGTGAGAGGCGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGGAAAGAAATTA 1203  
Db 1507 CTTTGTGAGAGGCGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGGAAAGAAATTA 1566  
QY 1204 ATGTTGATTAATAATAGATACACGCTAGTTTCAGAGTTACCATGTACGTATTCACATGAC 1263  
Db 1567 ATGTTGATTAATAATAGATACACGCTAGTTTCAGAGTTACCATGTACGTATTCACATGAC 1626  
QY 1264 TGGTTCCTGTATTTTCAGTCTTTCGATACGCTTAGGCTATGTCAAGTACAGGAAAAAA 1323  
Db 1627 TGGTTCCTGTATTTTCAGTCTTTCGATACGCTTAGGCTATGTCAAGTACAGGAAAAAA 1686  
QY 1324 CTGTGCAAGTACGACCTGATTCGCTTGCCTTGCCTTAACCTAAAGTCCATGTCCTGGG 1383  
Db 1687 CTGTGCAAGTACGACCTGATTCGCTTGCCTTGCCTTAACCTAAAGTCCATGTCCTGGG 1746  
QY 1384 CCTAAATCGTATAAATCTGATTTTTTTTTTTTTTTTTTTTTTTTCTCATATTCACATATGTA 1443  
Db 1747 CCTAAATCGTATAAATCTGATTTTTTTTTTTTTTTTTTTTTTTTCTCATATTCACATATGTA 1806  
QY 1444 ACCAGAACATCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATGTTGCTATGAT 1503  
Db 1807 ACCAGAACATCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATGTTGCTATGAT 1866  
QY 1504 TAACTTGTGCTGCTGATAGGACAGACTGGA 1536  
Db 1867 TAACTTGTGCTGCTGATAGGACAGACTGGA 1899

RESULT 14

ACA04166  
ID ACA04166 standard; cDNA; 2849 BP.  
XX  
AC ACA04166;  
XX  
DT 27-MAY-2003 (first entry)  
XX  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 285.  
XX  
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;  
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
KW infertility; birth defects; premature aging; AIDS; biosensor;  
KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
KW bioindicator; tumour.  
XX  
OS Homo sapiens.  
XX  
PN US2003032155-A1.

XX  
PD 13-FEB-2003.  
XX  
PF 03-MAY-2002; 2002US-0137865.  
XX  
PR 31-MAR-1997; 97WO-US05230.  
PR 12-JUN-1998; 98WO-US12456.  
PR 14-JUL-1998; 98WO-US14552.  
PR 28-AUG-1998; 98WO-US17888.  
PR 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19093.  
PR 14-SEP-1998; 98WO-US19094.  
PR 14-SEP-1998; 98WO-US19177.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 29-OCT-1998; 98WO-US22991.  
PR 29-OCT-1998; 98WO-US22992.  
PR 20-NOV-1998; 98WO-US24855.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 10-MAR-1999; 99WO-US05190.  
PR 20-APR-1999; 99WO-US08615.  
PR 14-MAY-1999; 99WO-US10733.  
PR 02-JUN-1999; 99WO-US12252.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 22-DEC-1999; 99WO-US30720.  
PR 30-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US0414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05746.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 30-MAY-2000; 2000WO-US14042.  
PR 02-JUN-2000; 2000WO-US14941.  
PR 28-JUL-2000; 2000WO-US15264.  
PR 11-AUG-2000; 2000WO-US20710.  
PR 23-AUG-2000; 2000WO-US22031.  
PR 24-AUG-2000; 2000WO-US23522.  
PR 08-NOV-2000; 2000WO-US23328.  
PR 10-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.

PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 22-JUN-2001; 2001WO-US20116.  
PR 23-JUN-2001; 2001WO-US21056.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 20-DEC-2000; 2000US-0747259.  
PR 28-FEB-2001; 2001US-0796498.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0806889.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 18-MAY-2001; 2001US-0860216.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 01-JUN-2001; 2001US-0872035.  
PR 05-JUN-2001; 2001US-0874503.  
PR 14-JUN-2001; 2001US-0882636.  
PR 19-JUN-2001; 2001US-0886342.  
PR 21-JUN-2001; 2001US-0887879.  
PR 18-JUL-2001; 2001US-0908827.  
PR 08-AUG-2001; 2001US-0924419.  
PR 09-AUG-2001; 2001US-0927796.  
PR 16-AUG-2001; 2001US-0931836.  
PR 19-DEC-2001; 2001US-0028072.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX WPI: 2003-331925/31.  
DR P-PSDB: ABU66988.  
XX  
XX New secreted and transmembrane nucleic acids and polypeptides,  
PT designated as PRO, useful for treating inflammation, organ failure,  
PT atherosclerosis, cardiac injury, infertility, birth defects, premature  
PT aging, AIDS, or cancer -  
XX  
XX Claim 2; Fig 285; 659pp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising, or which is  
CC at least 80% identical to, or the full-length coding sequence of, any of  
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide  
CC (one of 275 secreted or transmembrane proteins). The nucleic acid  
CC further comprises the full-length coding sequence of the DNA deposited  
CC under American Type Culture Collection (ATCC) accession number in a list  
CC given in the specification. Also included are vectors and host  
CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO  
CC antibodies, PRO extracellular domains and mature sequences, methods  
CC of detecting PRO proteins, methods for stimulating the release of  
CC TNF-alpha (tumour necrosis factor alpha) from human blood,  
CC (and the proliferation of differentiation of chondrocyte cells, the  
CC proliferation of, or gene expression in pericyte cells, the release or  
CC proteoglycans from cartilage, proliferation of inner ear utricular  
CC supporting cells, the proliferation of T-lymphocyte cells, the release  
CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the  
CC proliferation of endothelial cells), a method for modulating the uptake  
CC of glucose or free fatty acid (FFA) by skeletal muscle cells,  
CC a method for inhibiting the binding of A-peptide to factor VIIA,  
CC or the differentiation of adipocyte cells, a method for detecting the  
CC presence of a tumour in a mammal and an oligonucleotide probe derived  
CC from any of the nucleotide sequences cited above. The nucleic acids and  
CC polypeptides are useful for treating inflammatory diseases, organ  
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,  
CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or

CC diabetic complications. The nucleic acids are useful as hybridisation  
CC probes, in chromosome and gene mapping, and in generating antisense RNA  
CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
CC biosensors or bioreactors. Both are useful in tissue typing.  
CC The present sequence encodes a PRO protein of the invention.  
XX  
SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;  
Query Match 99.8%; Score 1532.6; DB 25; Length 2849;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GTAAATCCAGTTTTCAGCAACAAGGAAACAGACGAGTACAGATCCTCAGCATGAGA 63  
DB GTAAATCCAGTTTTCAGCAACAAGGAAACAGACGAGTACAGATCCTCAGCATGAGA 426  
QY 64 GAATTATTACTGTCTTACTTAATGGAGTATTCACAGCCCAAGTTTCTCATATCTATC 123  
DB GAATTATTACTGTCTTACTTAATGGAGTATTCACAGCCCAAGTTTCTCATATCTATC 486  
QY 124 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 183  
DB CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 546  
QY 184 TTACGTTTGTATGAAGAATTTGGGCTTGAAGACCAGAGATGACATATGCAAGTATGATT 243  
DB TTACGTTTGTATGAAGAATTTGGGCTTGAAGACCAGAGATGACATATGCAAGTATGATT 606  
QY 244 TTGTAGAAAGTTGGAGAACCCAGTATGGAATCTATTTAGGGCGCTGGTGTCTGGTA 303  
DB TTGTAGAAAGTTGGAGAACCCAGTATGGAATCTATTTAGGGCGCTGGTGTCTGGTA 666  
QY 304 CTGTACCAGGAAACAGATTTCTAAAGGAAATCAATTTAGGATAGATTTGTATCTGATG 363  
DB CTGTACCAGGAAACAGATTTCTAAAGGAAATCAATTTAGGATAGATTTGTATCTGATG 726  
QY 364 AATATTTTCTTGTGAACACAGGGTTCTGCATCCACTACACATTTGTCATGCCAATTTCA 423  
DB AATATTTTCTTGTGAACACAGGGTTCTGCATCCACTACACATTTGTCATGCCAATTTCA 786  
QY 424 CAGAAAGCTGTAGTCCTTTCAGTGTCTACCCCTTTCAGCTTTGCCACTGGACCTGTCTAATA 483  
DB CAGAAAGCTGTAGTCCTTTCAGTGTCTACCCCTTTCAGCTTTGCCACTGGACCTGTCTAATA 846  
QY 484 ATGCTATAAATCGCTTTAGTACCTTGAAGACCTTTATTCGATATCTTGAACACAGAGAT 543  
DB ATGCTATAAATCGCTTTAGTACCTTGAAGACCTTTATTCGATATCTTGAACACAGAGAT 906  
QY 544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTTTGGCAAGGCTTTTG 603  
DB GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTTTGGCAAGGCTTTTG 966  
QY 604 TTTTGGAGGAAATCCAGAGTGTGGATCTGAACCTTCTAAACAGAGAGGTAAAGATTAT 663  
DB TTTTGGAGGAAATCCAGAGTGTGGATCTGAACCTTCTAAACAGAGAGGTAAAGATTAT 1026  
QY 664 ACAGCTGCACACCTCGTAACTTTCAGTGTCCATAAGGAGAGAACTAAAGAGAACCGATA 723  
DB ACAGCTGCACACCTCGTAACTTTCAGTGTCCATAAGGAGAGAACTAAAGAGAACCGATA 1086  
QY 724 CCATTTTTCGCCAGGTTGTCTCTCTGTTAAACCTGTGGTGGGAACTGTGCTGTTGTC 783  
DB CCATTTTTCGCCAGGTTGTCTCTCTGTTAAACCTGTGGTGGGAACTGTGCTGTTGTC 1146  
QY 784 TCCCAATTTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTTACTAAAAAATACCACGAGG 843  
DB TCCCAATTTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTTACTAAAAAATACCACGAGG 1206  
QY 844 TCCTTTAGTTGAGACCAAAACCCGGTGTGAGGGGATTCACAAATCACTACCGACGTGG 903  
DB TCCTTTAGTTGAGACCAAAACCCGGTGTGAGGGGATTCACAAATCACTACCGACGTGG 1266  
QY 904 CCCTGGAGCACCATGAGAGGTGTGACTGTGTGTGAGAGGGAGCACAGGAGATAGCCGC 963





PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 22-JUN-2001; 2001WO-US20116.  
PR 23-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 20-DEC-2000; 2000US-0747259.  
PR 28-FEB-2001; 2001US-0796498.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 18-MAY-2001; 2001US-0860216.  
PR 25-MAY-2001; 2001US-0866028.  
PR 01-JUN-2001; 2001US-0872035.  
PR 05-JUN-2001; 2001US-0874503.  
PR 14-JUN-2001; 2001US-0882636.  
PR 19-JUN-2001; 2001US-0886342.  
PR 21-JUN-2001; 2001US-0887879.  
PR 18-JUL-2001; 2001US-0908827.  
PR 06-AUG-2001; 2001US-0924419.  
PR 09-AUG-2001; 2001US-0927796.  
PR 16-AUG-2001; 2001US-0931836.  
PR 19-DEC-2001; 2001US-0028072.  
PR  
XX (GETH ) GENENTECH INC.

PA Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX

XX WPI: 2003-148238/14.

XX P-PSDB; ABUS9793.

XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
XX are therapeutically useful for enhancing immune response and in cancer  
XX treatments -

XX Claim 2; Fig 285; 659pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO  
XX polypeptides are useful in detecting PRO polypeptides in a sample, in  
XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
XX in modulating at least one biological activity of a cell expressing a PRO  
XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
XX stimulate adrenal cortical capillary endothelial growth, and PRO536,  
XX PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
XX useful for treating conditions or disorders where angiogenesis would be  
XX beneficial, e.g. wound healing and antagonist of this polypeptide are  
XX useful for treating cancerous tumours. PRO812 inhibits vascular  
XX endothelial growth factor (VEGF) stimulated proliferation of endothelial  
XX cells and is thus useful for inhibiting endothelial cell growth in  
XX mammals which would be beneficial in inhibiting tumour growth. PRO826,  
XX PRO1068, PRO1184, and PRO1375 stimulate proliferation of  
XX stimulated T-lymphocytes and are therapeutically useful for enhancing  
XX immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of  
XX retinal neurons cells (PRO132 is also enhances survival/proliferation of  
XX rod photoreceptor cells) and therefore are useful for treating retinal  
XX disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
XX and PRO11066 induce proliferation of mammalian kidney mesangial cells,  
XX and therefore are useful for treating kidney disorders associated with  
XX decreased mesangial cell function such as Berger disease or other  
XX nephropathies associated with dermatitis, Herpetiformis or Crohn's  
XX disease. PRO310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
XX proliferation and/or redifferentiation of chondrocytes in culture and  
XX are thus useful for treating sports injuries, and arthritis. This  
XX sequence encodes a novel human PRO protein.

SQ	Sequence	2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;
	Query Match	99.8%; Score 1532.6; DB 25; Length 2849;
	Best Local Similarity	99.9%; Pred. No. 0;
	Matches 1532; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
Qy	4	GTAATTCAGTTTCCAGCAACAAGGACAGAACGAGTACAGATCCTCAGCATGAGA 63
Db	367	GTAATTCAGTTTCCAGCAACAAGGACAGAACGAGTACAGATCCTCAGCATGAGA 426
Qy	64	GAATTTACTGTGTCTACTAAATGGAAGTATTCACAGCCCAAGTTTCTCATCTATTC 123
Db	427	GAATTTACTGTGTCTACTAAATGGAAGTATTCACAGCCCAAGTTTCTCATCTATTC 486
Qy	124	CAAGAAATACGGTCTTCGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 183
Db	487	CAAGAAATACGGTCTTCGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 546
Qy	184	TTACGTTTGTATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
Db	547	TTACGTTTGTATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 606
Qy	244	TTGTAGAAGTTGAGAACCCAGTGTGGAACCTATATTAGGCGCTGGTGTGGTCTGTA 303
Db	607	TTGTAGAAGTTGAGAACCCAGTGTGGAACCTATATTAGGCGCTGGTGTGGTCTGTA 666
Qy	304	CTGTACCAGGAAACAGATTTCTAAAGAAATCAATTAAGATAAGATTTCTATCTGATG 363
Db	667	CTGTACCAGGAAACAGATTTCTAAAGAAATCAATTAAGATAAGATTTCTATCTGATG 726
Qy	364	AATATTTTCTTCTGAACCCAGGGTCTTCATCCACTACAACATTTGTATGCCAATTCAT 423
Db	727	AATATTTTCTTCTGAACCCAGGGTCTTCATCCACTACAACATTTGTATGCCAATTCAT 786
Qy	424	CAGAAGCTGTGAGTCTTTCAGTGTACCCCTTTCAGCTTTCAGCTGACCTGCTTAATA 483
Db	787	CAGAAGCTGTGAGTCTTTCAGTGTACCCCTTTCAGCTTTCAGCTGACCTGCTTAATA 846
Qy	484	ATGCTATAACTGCTTTAGTACCTTGAAGACCTTATTTCGATATCTTCAACACAGAGAT 543
Db	847	ATGCTATAACTGCTTTAGTACCTTGAAGACCTTATTTCGATATCTTCAACACAGAGAT 906
Qy	544	GGCAGTTTGGACTTAGAAGATCTATATAGGCCAACTTGTGCAACTTCTTGGCAAGGCTTTTG 603
Db	907	GGCAGTTTGGACTTAGAAGATCTATATAGGCCAACTTGTGCAACTTCTTGGCAAGGCTTTTG 966
Qy	604	TTTTTGGNAGAAATCCAGAGTGTGGTCTGAACCTTCTAACAGAGAGGTAGATTAT 663
Db	967	TTTTTGGNAGAAATCCAGAGTGTGGTCTGAACCTTCTAACAGAGAGGTAGATTAT 1026
Qy	664	ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGGATA 723
Db	1027	ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGGATA 1086
Qy	724	CCATTTTCTGCCAGGTTGTCTCCTGGTTAAACCGTGTGGTGGGAATCTGTGCTGTGTC 783
Db	1087	CCATTTTCTGCCAGGTTGTCTCCTGGTTAAACCGTGTGGTGGGAATCTGTGCTGTGTC 1146
Qy	784	TCCCAATTTCAATGAATGTCAATGTGTCCCAAGCAAGTTTACTTAAAAATACCAACGAGG 843
Db	1147	TCCCAATTTCAATGAATGTCAATGTGTCCCAAGCAAGTTTACTTAAAAATACCAACGAGG 1206
Qy	844	TCCTTTCAGTTGAGAACCAASACCGGTGTGAGGGGATGTCACAAATCACTACCCACGCTGG 903
Db	1207	TCCTTTCAGTTGAGAACCAAGCCGGTGTGAGGGGATGTCACAAATCACTACCCACGCTGG 1266
Qy	904	CCCTTGGAGCACTAGAGAGTGTGACTGTGTGTGTCAGAGGGAGCACAGGAGATAGCCGC 963
Db	1267	CCCTTGGAGCACTAGAGAGTGTGACTGTGTGTGTCAGAGGGAGCACAGGAGATAGCCGC 1326
Qy	964	ATCACCAACCAAGCTCTTGGCCAGAGCTGTGTCAGTGGCTGATTTCTATTAGAGAA 1023
Db	1327	ATCACCAACCAAGCTCTTGGCCAGAGCTGTGTCAGTGGCTGATTTCTATTAGAGAA 1386

QY	1024	CGTATGCGTTATCTCCATCCTTAATCTCAGTTCTTTGCTTCAAGGACCTTTTCATCTTCAG	1083
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QY	1084	GATTTACAGTGCATTCTGAAAGAGGAGACATCAACAGATTAGGAGTTGTGCAACAGCT	1143
Db	1447	GATTTACAGTGCATTCTGAAAGAGGAGACATCAACAGATTAGGAGTTGTGCAACAGCT	1506
QY	1144	CTTTTGAGAGGAGGCTTAAAGGACAGGAGAAAGGCTCTTCAATCGTGGAAAGAAATTA	1203
Db	1507	CTTTTGAGAGGAGGCTTAAAGGACAGGAGAAAGGCTCTTCAATCGTGGAAAGAAATTA	1566
QY	1204	ATGTTGTATTAAATAGATCACCGCTAGTTTCAGAGTTACCATGTACGTATTCACCTAGC	1263
Db	1567	ATGTTGTATTAAATAGATCACCGCTAGTTTCAGAGTTACCATGTACGTATTCACCTAGC	1626
QY	1264	TGGGTTCTGTATTCTCAGTTCTTTCGATACGCTTAGGGTAAATGTCAGTACAGGAAAAA	1323
Db	1627	TGGGTTCTGTATTCTCAGTTCTTTCGATACGCTTAGGGTAAATGTCAGTACAGGAAAAA	1686
QY	1324	CTGTGCAAGTGAGCACCTGATTCGTTGCCCTTGCTTAACTCTAAAGCTCCATGTCTCTGG	1383
Db	1687	CTGTGCAAGTGAGCACCTGATTCGTTGCCCTTGCTTAACTCTAAAGCTCCATGTCTCTGG	1746
QY	1384	CCTAAAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTTTTTGTGCTCATATTCA	1443
Db	1747	CCTAAAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTTTTTGTGCTCATATTCA	1806
QY	1444	ACCAGAACATTCATGTACTACAAACCTGGTCTTTTAAAGGAACTATGTTGCTATGAAT	1503
Db	1807	ACCAGAACATTCATGTACTACAAACCTGGTCTTTTAAAGGAACTATGTTGCTATGAAT	1866
QY	1504	TAAACTTGTCATGCTGTAGTACAGACTGGA	1536
Db	1867	TAAACTTGTCATGCTGTAGTACAGACTGGA	1899

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Job time : 287.611 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 23:46:56 ; Search time 75.0293 Seconds  
(without alignments)  
9035.995 Million cell updates/sec

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Perfect score: 1536  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Capext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	1532.6	99.8	2825	4	US-09-265-886-1
3	1511	98.4	1760	4	US-09-564-595D-32
4	1511	98.4	1760	4	US-09-706-968-1
5	1497	97.5	1764	4	US-09-457-066-1
6	955.6	62.2	1095	4	US-09-457-066-50
7	955.6	62.2	1095	4	US-09-706-968-50
8	721	46.9	3571	4	US-09-564-595D-34
9	721	46.9	3571	4	US-09-706-968-42
10	721	46.9	3573	4	US-09-457-066-42
11	684.4	44.6	1035	4	US-09-457-066-6
12	684.4	44.6	1035	4	US-09-706-968-6
13	177.4	11.5	1110	4	US-09-564-595D-6
14	117.4	7.6	1472	4	US-09-540-224-3
15	117.4	7.6	1472	4	US-09-564-595D-52
16	103.6	6.7	1882	4	US-09-540-224-1
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18	103.6	6.7	1882	4	US-09-706-968-36
19	102.4	6.7	1910	4	US-09-457-066-36
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21	40	2.6	40	4	US-09-040-220D-4
22	40	2.6	40	4	US-09-265-886-4
23	37.2	2.4	3098	1	US-08-447-500-1
24	37.2	2.4	3098	1	US-08-454-097-1
25	37.2	2.4	3098	1	US-08-447-408-1
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ALIGNMENTS

RESULT 1  
US-09-040-220D-1  
; Sequence 1, Application US/09040220D  
; Patent No. 6391311  
; GENERAL INFORMATION:  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Kuo, Sophia S.  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR  
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC  
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,  
; TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION  
; FILE REFERENCE: P1122  
; CURRENT APPLICATION NUMBER: US/09/040,220D  
; CURRENT FILING DATE: 1998-03-17  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 1  
; LENGTH: 2825  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: Human  
; LOCATION: 2689  
; OTHER INFORMATION: N is A, T, C or G  
US-09-040-220D-1

Query Match	99.8%;	Score 1532.6;	DB 4;	Length 2825;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1532;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	4	GTAATTCAGTTTCCAGCAACAGGACAGACAGGAGTACAGATCCTCAGCATGAGA	63	
Db	341	GTAATTCAGTTTCCAGCAACAGGACAGGAGTACAGATCCTCAGCATGAGA	400	
Qy	64	GAATATTACTGTGTCTACTTAATGGAAGTATTCACGCCCAAGTTTCTCATCTTATC	123	
Db	401	GAATATTACTGTGTCTACTTAATGGAAGTATTCACGCCCAAGTTTCTCATCTTATC	460	
Qy	124	CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAC	183	
Db	461	CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAC	520	
Qy	184	TTAGCTTTGATGAAGATTGGGCTTCAGACCCAGAGATGACATATGCAAGTATGATT	243	
Db	521	TTAGCTTTGATGAAGATTGGGCTTCAGACCCAGAGATGACATATGCAAGTATGATT	580	
Qy	244	TTGTAGAAGTTGAGGACCCAGTGCATGATGAACTATTATAGGGCGCTGGTGTCTGGTA	303	
Db	581	TTGTAGAAGTTGAGGACCCAGTGCATGATGAACTATTATAGGGCGCTGGTGTCTGGTA	640	
Qy	304	CTGTACCAGGAAAACAGATTCTTAAGGAAATCAATAGATAAGATTCTATCTGATG	363	

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364	Qy	AAATATTTCTCTGTGAACACGAGGTTCTG	CATCCACATACAA	CATTTGTCATGCCACAATTCA	423		
701	Db	AAATATTTCTCTGTGAACACGAGGTTCTG	CATCCACATACAA	CATTTGTCATGCCACAATTCA	760		
424	Qy	CAGAAGCTGTGAGTCTT	CAGTGTACCCCTTCAGCTTTGCCAC	TGGACCTGCTTTAA	483		
761	Db	CAGAAGCTGTGAGTCTT	CAGTGTACCCCTTCAGCTTTGCCAC	TGGACCTGCTTTAA	820		
484	Qy	ATGCTATAACTGCTTT	TAGTACCTTGGAGACCTTATTCGATATCTT	TGAACACAGAGAT	543		
821	Db	ATGCTATAACTGCTTT	TAGTACCTTGGAGACCTTATTCGATATCTT	TGAACACAGAGAT	880		
544	Qy	GGCAGTTGGACTTT	ATAGAGATCTATATAGGCCAACTTTGGCAAC	CTTTCTTGGCAAGCTTTTG	603		
881	Db	GGCAGTTGGACTTT	ATAGAGATCTATATAGGCCAACTTTGGCAAC	CTTTCTTGGCAAGCTTTTG	940		
604	Qy	TTTTTTGGAAGAAATCCAGAGTGTG	GATCTGTAACCTTTCTAA	CAGAGGAGGTAA	663		
941	Db	TTTTTTGGAAGAAATCCAGAGTGTG	GATCTGTAACCTTTCTAA	CAGAGGAGGTAA	1000		
664	Qy	ACAGCTGCACACCTCGTAAC	TTTCAGTGTCCATAAGGGAAGAACTTAA	AGAGAACCGATA	723		
1001	Db	ACAGCTGCACACCTCGTAAC	TTTCAGTGTCCATAAGGGAAGAACTTAA	AGAGAACCGATA	1060		
724	Qy	CCATTTTCTGGCCAGGTTGCTCTCGTGTAA	ACGCTGTGGGAACTGTGCTGTGTC	783			
1061	Db	CCATTTTCTGGCCAGGTTGCTCTCGTGTAA	ACGCTGTGGGAACTGTGCTGTGTC	1120			
784	Qy	TCCACAAATTCGAATGAATGTCAAT	TGTTCCCAAGCAAAAGTTATCTAA	AAAAATACCA	843		
1121	Db	TCCACAAATTCGAATGAATGTCAAT	TGTTCCCAAGCAAAAGTTATCTAA	AAAAATACCA	1180		
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1181	Db	TCCTTCAGTTGAGNCCAAASACCGGTGT	CAGGGATTGCAAAATCTAC	CCACGAGTGG	1240		
904	Qy	CCCTGGAGCACCATGAGGAGTGTCACT	TGTGTGCAGAGGAGCACAGGAGGATAG	CGCG	963		
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1084	Qy	GATTTACAGTGCATTTCTGAAAGAGGAG	ACATCAAAACAGAAATTAGGAGTTGTG	CAACAGCT	1143		
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Db	1781	ACCAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACCTATGTTGCTATGAAT	1840
Qy	1504	TAAACTTGTCATGCTGATAGCAGACACTGGA	1536
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RESULT 2

US-09-265-686-1

; Sequence 1, Application US/09265686

; Patent No. 6455283

; GENERAL INFORMATION:

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Kuo, Sophia S.

; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND EMPI

; FILE REFERENCE: P1122P2

; CURRENT APPLICATION NUMBER: US/09/265,686

; CURRENT FILING DATE: 1999-03-10

; PRIOR APPLICATION NUMBER: US 09/040,220

; PRIOR FILING DATE: 1998-03-17

; PRIOR APPLICATION NUMBER: US 09/184,216

; PRIOR FILING DATE: 1998-11-02

; NUMBER OF SEQ ID NOS: 8

; SEQ ID NO 1

; LENGTH: 2825

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: Unknown

; LOCATION: 2689

; OTHER INFORMATION: Any nucleotide

US-09-265-686-1

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Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1532;	Conservative	1;	Mismatches	0;
			Indels	Gaps
Qy	4	GTAAATCCAGTTTCCAGCAACAAGGACAGAACGGAGTACAGATCTCTCAGCATGAGA	63	
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Qy	64	GAATTATTACTGTGCTACTAAATGGAAGTATTCACAGCCCCAAGGTTTCCCTCATCTTATC	123	
Db	401	GAATTATTACTGTGCTACTAAATGGAAGTATTCACAGCCCCAAGGTTTCCCTCATCTTATC	460	
Qy	124	CAAGAAATACGGTCTTGSTATGGAGATTAGTAGCAGTAGAGGAAAAATGTATGGATACAAC	183	
Db	461	CAAGAAATACGGTCTTGSTATGGAGATTAGTAGCAGTAGAGGAAAAATGTATGGATACAAC	520	
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Qy	244	TTGTAGAAGTTGAGGAACCCAGTGTGGAACTATATTAGGCGCTGGTGGTTCTGGTA	303	
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Qy	304	CTGTACCAGGAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG	363	
Db	641	CTGTACCAGGAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG	700	
Qy	364	AATATTTTCTCTGAACCAAGGTTCTGCATCCCATACAACATTTGTATGCCAATTC	423	
Db	701	AATATTTTCTCTGAACCAAGGTTCTGCATCCCATACAACATTTGTATGCCAATTC	760	
Qy	424	CAGAAGCTGTAGTCTCTAGTGGTACCCCTTTGAGTTTGCACCTGTGACCTGCTTAATA	483	
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QY 484 ATGCTATAAATGCGCTTTAGTACCTTTGGAAGACCTTATTTCGATATCTTGAACCAAGAGAT 543
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QY 544 GGCAGTTGGACTTAGAGATCTATATAGGCCAACTTGCGCAACTCTTGGCAAGCTTTTG 603
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Db 1841 TAAACTTGTGTCTGTGATAGGACAGACTGGA 1873
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RESULT 3
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; Sequence 32, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGP4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-564-595D-32
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Query Match 98.4%; Score 1511; DB 4; Length 1760;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1522; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

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Db 236 GTAAATTCAGTTCCTGATTTCCAGCAACCAAGGAAACAGAACGAGTACAAATCCTCAGCATGAGA 295
QY 64 GAAATTTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATCTTATTC 123
Db 296 GAAATTTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATCTTATTC 355
QY 124 CAAGAAATACCGTCTTGGTATGGAGATTTAGTAGCAGTACAGGAAATATGATGGATACAAAC 183
Db 356 CAAGAAATACCGTCTTGGTATGGAGATTTAGTAGCAGTACAGGAAATATGATGGATACAAAC 415
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Db 656 CAGAAGCTGTGAGTCTTTCAGTGTACCCCTTTCAGCTTTGCCACTGCCACTGCTGCTTAATA 715
QY 484 ATGCTATAAATGCGCTTTAGTACCTTTGGAAGACCTTATTTCGATATCTTGAACCAAGAGAT 543
Db 716 ATGCTATAAATGCGCTTTAGTACCTTTGGAAGACCTTATTTCGATATCTTGAACCAAGAGAT 775
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Db 836 TTTTGGAGAAAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGAGTAAAGATTAT 895
Qy 664 ACAGCTGCACCTCTGTAACCTTCTAGTGTCTTAAGGGAAGAACTAAAGAGACCGATA 723
Db 896 ACAGCTGCACCTCTGTAACCTTCTAGTGTCTTAAGGGAAGAACTAAAGAGACCGATA 955
Qy 724 CCAATTTCTGCCAGGTGTCTCTCTGGTTAAACCGTGTGGTGGAACTGTCCCTGTTGTC 783
Db 956 CCAATTTCTGCCAGGTGTCTCTCTGGTTAAACCGTGTGGTGGAACTGTCCCTGTTGTC 1015
Qy 784 TCCCAATGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAATACCAAGAGG 843
Db 1016 TCCCAATGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAATACCAAGAGG 1075
Qy 844 TCCCTCAGTTGAGACCAAAACCGGTGTCAAGGGAATTCACAAATCACTCACCGACGTGG 903
Db 1076 TCCCTCAGTTGAGACCAAAACCGGTGTCAAGGGAATTCACAAATCACTCACCGACGTGG 1135
Qy 904 CCCTGGAGCACATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGATAGCCGC 963
Db 1136 CCCTGGAGCACATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGATAGCCGC 1195
Qy 964 ATCAACCAAGAGCTCTTGGCCAGAGCTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAG 1023
Db 1196 ATCAACCAAGAGCTCTTGGCCAGAGCTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAG 1255
Qy 1024 CGTATGCGTTATCTCCATCTTAACTCAGTTGTTGCTTCAAGACCTTTCATCTTCAG 1083
Db 1256 CGTATGCGTTATCTCCATCTTAACTCAGTTGTTGCTTCAAGACCTTTCATCTTCAG 1315
Qy 1084 GATTTACAGTGCATTTCTGAAAGAGAGACATCAAAACAGAAATAGGAGTGTGCAACAGCT 1143
Db 1316 GATTTACAGTGCATTTCTGAAAGAGAGACATCAAAACAGAAATAGGAGTGTGCAACAGCT 1375
Qy 1144 CTTTGGAGAGGCTTAAAGACAGAGAGAAAGTCTTCAATCGTGAAGAAATTAATTA 1203
Db 1376 CTTTGGAGAGGCTTAAAGACAGAGAGAAAGTCTTCAATCGTGAAGAAATTAATTA 1435
Qy 1204 ATGTTGTAATTAATAGATCACCAGCTAGTTTTCAGAGTTTACCAGTATTCACACTAGC 1263
Db 1436 ATGTTGTAATTAATAGATCACCAGCTAGTTTTCAGAGTTTACCAGTATTCACACTAGC 1495
Qy 1264 TGGGTTCTGTATTTTCAGTCTTTTCGATACCGCTTAGGGTAATGTGCAAGTACAGGAAAAA 1323
Db 1496 TGGGTTCTGTATTTTCAGTCTTTTCGATACCGCTTAGGGTAATGTGCAAGTACAGGAAAAA 1555
Qy 1324 CTGTGCAAGTGCACCTGATTCGGTTCGCTTGAATCTTAAAGCTCCATGTCCTGGG 1383
Db 1556 CTGTGCAAGTGCACCTGATTCGGTTCGCTTGAATCTTAAAGCTCCATGTCCTGGG 1615
Qy 1384 CCTAAAATCGTATAAAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTTTTCATATGTA 1442
Db 1616 CCTAAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTTTTTTTTCATATGTA 1675
Qy 1443 AACAGAACTATGATGATCAAAACCTGTTTTTAAAGGAACTAGTGTGCTATGAA 1502
Db 1676 AACAGAACTATGATGATCAAAACCTGTTTTTAAAGGAACTATGTTGCTATGAA 1735
Qy 1503 TTAAACTGTGTCATGCTGATAGGA 1527
Db 1736 TTAAACTGTGTCGTCGATAGGA 1760
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## RESULT 4

US-09-706-968-1

; Sequence 1, Application US/09706968

; Patent No. 6528050

; GENERAL INFORMATION:

; APPLICANT: Gao, Zeren

; APPLICANT: Hart, Charles E.

; APPLICANT: Piddington, Christopher S.

```
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVBGF3
; FILE REFERENCE: 98-60CI
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-706-968-1
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Query Match 98.4%; Score 1511; DB 4; Length 1760;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1522; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
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Qy 4 GTAAATTCAGTTTCCAGCAACAAAGGAACAGAGTACAGATCCTCAGCATGAGA 63
Db 236 GTAAATTCAGTTTCCAGCAACAAAGGAACAGAGTACAGATCCTCAGCATGAGA 295
Qy 64 GAATATTACTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCATACTATC 123
Db 296 GAATATTACTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCATACTATC 355
Qy 124 CAAGAAATACCGTCTTGGTATGAGATTAGTAGAGAGAGAAATGTATGGATACAC 183
Db 356 CAAGAAATACCGTCTTGGTATGAGATTAGTAGAGAGAGAAATGTATGGATACAC 415
Qy 184 TTACGTTTGAATGAAGATTTCGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
Db 416 TTACGTTTGAATGAAGATTTCGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 475
Qy 244 TTGTAGAGTTGAGAACCCAGTGTATGAACTATATATTAGGGCGCTGTGTCTGTTA 303
Db 476 TTGTAGAGTTGAGAACCCAGTGTATGAACTATATATTAGGGCGCTGTGTCTGTTA 535
Qy 304 CTGTACAGGAGAAACAGAGTTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 363
Db 536 CTGTACAGGAGAAACAGAGTTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 595
Qy 364 AATATTTTCTTGAACCCAGGTTCTGCATCCACTACAACTTGTCTATGCCACAATTCA 423
Db 596 AATATTTTCTTGAACCCAGGTTCTGCATCCACTACAACTTGTCTATGCCACAATTCA 655
Qy 424 CAGAGCTGTGAGTCCCTTTCAGTGTACCCCTTTCAGCTTTCACCTGACCTGCTTAATA 483
Db 656 CAGAGCTGTGAGTCCCTTTCAGTGTACCCCTTTCAGCTTTCACCTGACCTGCTTAATA 715
Qy 484 ATGCTATAAATCGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTGAACCCAGAGAT 543
Db 716 ATGCTATAAATCGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTGAACCCAGAGAT 775
Qy 544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGGCAACTTCTTGGCAAGGCTTTTG 603
Db 776 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGGCAACTTCTTGGCAAGGCTTTTG 835
Qy 604 TTTTGGAGAAAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGAGGTTAAGATTAT 663
Db 836 TTTTGGAGAAAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGAGGTTAAGATTAT 895
Qy 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 723
Db 896 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 955
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QY 724 CCATTTTCTGCCAGGTTGCTCTCTGTTAAACGCTGTGTGGAACTGTGCTGTGTC 783
Db 956 CCATTTTCTGCCAGGTTGCTCTCTGTTAAACGCTGTGTGGAACTGTGCTGTGTC 1015
QY 784 TCCACAAATGCAATGAATGCAATGTGTCCCAAGCAAGTTTACTAAAAATACCACGAGG 843
Db 1016 TCCACAAATGCAATGAATGCAATGTGTCCCAAGCAAGTTTACTAAAAATACCACGAGG 1075
QY 844 TCCCTTCAGTTGAGACCAAAACCGGTTGTCAGGGGATTTGCAAAATCACTCCACGACGTTG 903
Db 1076 TCCCTTCAGTTGAGACCAAAACCGGTTGTCAGGGGATTTGCAAAATCACTCCACGACGTTG 1135
QY 904 CCCTGAGACCAATGAGAGTGTGACTGTGTGTCAGAGGAGACACAGGAGTAGCCGC 963
Db 1136 CCCTGAGACCAATGAGAGTGTGACTGTGTGTCAGAGGAGACACAGGAGTAGCCGC 1195
QY 964 ATCACCCACGACGCTCTTGCACAGAGCTGTGCAAGTGTGAGTGTGCTTATTATAGAGAA 1023
Db 1196 ATCACCCACGACGCTCTTGCACAGAGCTGTGCAAGTGTGAGTGTGCTTATTATAGAGAA 1255
QY 1024 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTGCTTCAAGGACCTTTCATCTTCAG 1083
Db 1256 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTGCTTCAAGGACCTTTCATCTTCAG 1315
QY 1084 GATTTCAGTGCATCTGAAGAGAGACATCAACAGAAATAGAGTTGTGCAACAGCT 1143
Db 1316 GATTTCAGTGCATCTGAAGAGAGACATCAACAGAAATAGAGTTGTGCAACAGCT 1375
QY 1144 CTTTGTGAGAGAGGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGAAGAAATTA 1203
Db 1376 CTTTGTGAGAGAGGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGAAGAAATTA 1435
QY 1204 ATGTTGTATTAATAGATCACAGCTAGTTTCAGAGTTTACCATGTACGATTTCCACTAGC 1263
Db 1436 ATGTTGTATTAATAGATCACAGCTAGTTTCAGAGTTTACCATGTACGATTTCCACTAGC 1495
QY 1264 TGGGTTCTGTATTTTCAAGTCTTTCGATACGCTTAGGGTAATGTACGATACAGGAA 1323
Db 1496 TGGGTTCTGTATTTTCAAGTCTTTCGATACGCTTAGGGTAATGTACGATACAGGAA 1555
QY 1324 CTGTGCAAGTACGACACCTGATTCGTTGCTTAACTCTTAAAGCTCCATGTCTGGG 1383
Db 1556 CTGTGCAAGTACGACACCTGATTCGTTGCTTAACTCTTAAAGCTCCATGTCTGGG 1615
QY 1384 CTTAAATTCGTATTAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTA 1442
Db 1616 CTTAAATTCGTATTAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTA 1675
QY 1443 AACAGACATCTATGTACTACAAACCTGTTTAAAGGAACTATGTGCTATGAA 1502
Db 1676 AACAGACATCTATGTACTACAAACCTGTTTAAAGGAACTATGTGCTATGAA 1735
QY 1503 TTAACCTTGTCTATGCTGATAGGA 1527
Db 1736 TTAACCTTGTCTGCTGATAGGA 1760
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## RESULT 5

US-09-457-066-1

; Sequence 1, Application US/09457066

; Patent No. 6432673

; GENERAL INFORMATION:

; APPLICANT: Gao, Zeren

; APPLICANT: Hart, Charles E.

; APPLICANT: Piddington, Christopher S.

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Shoemaker, Kimberly E.

; APPLICANT: Gilbertson, Debra G.

; APPLICANT: West, James W.

; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3

; FILE REFERENCE: 98-60

; CURRENT APPLICATION NUMBER: US/09/457,066

; CURRENT FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1760

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURES:

; NAME/KEY: CDS

; LOCATION: (154)...(1191)

US-09-457-066-1

Query Match 97.5%; Score 1497; DB 4; Length 1764;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1522; Conservative 1; Mismatches 1; Indels 5; Gaps 2;

QY 4 GTAAATTCAGTTTCCAGCAACAAAGGACGAGTACAGATCCTCAGCATGAGA 63

Db 236 GTAAATTCAGTTTCCAGCAACAAAGGACGAGTACAGATCCTCAGCATGAGA 295

QY 64 GAATTTACTGTGTCTACTTAATGGAAGTATTCACAGCCCAAGTTTCTCATCTTATC 123

Db 296 GAATTTACTGTGTCTACTTAATGGAAGTATTCACAGCCCAAGTTTCTCATCTTATC 355

QY 124 CAAGAAATACGCTCTTGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATCAAC 183

Db 356 CAAGAAATACGCTCTTGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATCAAC 415

QY 184 TTAGCTTTGATGAAAGATTTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243

Db 416 TTAGCTTTGATGAAAGATTTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 475

QY 244 TTGTAGAAGTTGAGGAAACCCAGTGTGAAACTATATATAGGCGCTGGTGTCTGTGTA 303

Db 476 TTGTAGAAGTTGAGGAAACCCAGTGTGAAACTATATATAGGCGCTGGTGTCTGTGTA 535

QY 304 CTGTACACGAGGAAACAGATTTCTAAAGGAAATCAAATTTAGGATAAGATTTGTATCTGATG 363

Db 536 CTGTACACGAGGAAACAGATTTCTAAAGGAAATCAAATTTAGGATAAGATTTGTATCTGATG 595

QY 364 AATATTTTCTTGAACACAGGTTTCTGCATCCACTACAACTTGTCTATGCCAATTC 423

Db 596 AATATTTTCTTGAACACAGGTTTCTGCATCCACTACAACTTGTCTATGCCAATTC 655

QY 424 CAGAGCTGTGAGTCTTTCAGTGTACCCCTTTCAGCTTGGCCACTGAGACCTGCTTAATA 483

Db 656 CAGAGCTGTGAGTCTTTCAGTGTACCCCTTTCAGCTTGGCCACTGAGACCTGCTTAATA 715

QY 484 ATGCTATAACTGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTGAACACAGAGAT 543

Db 716 ATGCTATAACTGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTGAACACAGAGAT 775

QY 544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTTTGGCAAGGCTTTTG 603

Db 776 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTTTGGCAAGGCTTTTG 835

QY 604 TTTTGGAGAGAAATCCAGAGTGTGGATCTGAACTTCTAAACAGAGGAGTAAAGATTAT 663

Db 836 TTTTGGAGAGAAATCCAGAGTGTGGATCTGAACTTCTAAACAGAGGAGTAAAGATTAT 895

QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCTCAGTGTCCATAAGGAGAACTTAAAGAGAACCGATA 723

Db 896 ACAGCTGCACACCTCGTAACTTCTCAGTGTCTCAGTGTCCATAAGGAGAACTTAAAGAGAACCGATA 955

QY 724 CCATTTTCTGCCAGGTTGCTCTCTGTTAAACGCTGTGTGGAACTGTGCTGTGTC 783

Db 956 CCATTTTCTGCCAGGTTGCTCTCTGTTAAACGCTGTGTGGAACTGTGCTGTGTC 1015

QY 784 TCCACAAATGCAATGAATGCAATGTGTCCCAAGCAAGTTTACTAAAAATACCACGAGG 843

Db 1016 TCCACAAATGCAATGAATGCAATGTGTCCCAAGCAAGTTTACTAAAAATACCACGAGG 1075

QY 844 TCCCTTCAGTTGAGACCAAAACCGGTTGTCAGGGGATTTGCAAAATCACTCCACGACGTTG 903



Db 1076 TCCTTCAGTTGAGACCAAGACCGGTGTCTGAGGGGATTCGACAAATCACTCACCGACGTGG 1135  
Qy 904 CCCTGGAGCCATGAGGAGTGACCTGTGTGTCAGAGGAGCAGACAGGAGGATAGCCGC 963  
Db 1136 CCCTGGAGCCATGAGGAGTGACCTGTGTGTCAGAGGAGCAGACAGGAGGATAGCCGC 1195  
Qy 964 ATACACACACGACGCTCTTGCCACAGAGCTGTGCAGT---GCACTGGCTGATTCATTATAG 1019  
Db 1196 ATACACACACGACGCTCTTGCCACAGAGCTGTGCAGTLYLYGACGTGGCTGATTCATTATAG 1255  
Qy 1020 AGAACGTATGCTTATCTCCATCTTAATCTCACTGCTGTGTGCTTCAAGGACCTTTCATCT 1079  
Db 1256 AGAACGTATGCTTATCTCCATCTTAATCTCACTGCTGTGTGCTTCAAGGACCTTTCATCT 1315  
Qy 1080 TCAGGATTTACAGTGCATCTTGAAGAGGAGACATCAAAAGAGATTTAGGAGTCTGCAAC 1139  
Db 1316 TCAGGATTTACAGTGCATCTTGAAGAGGAGACATCAAAAGAGATTTAGGAGTCTGCAAC 1375  
Qy 1140 AGCTCTTTTGAAGAGGAGGCTTAAAGGACAGGAGAAAGGCTTCAATCGTGGAAAGAAA 1199  
Db 1376 AGCTCTTTTGAAGAGGAGGCTTAAAGGACAGGAGAAAGGCTTCAATCGTGGAAAGAAA 1435  
Qy 1200 TTAATGTTGATTAATAGATCACACGAGTGTGTTTCAGAGTACCATGTACGTTATCCAC 1259  
Db 1436 TTAATGTTGATTAATAGATCACACGAGTGTGTTTCAGAGTACCATGTACGTTATCCAC 1495  
Qy 1260 TAGCTGGGTTCTGTATTTCACTTCTTCGATACCGCTTAGGGTAAATGTCACTACAGAAA 1319  
Db 1496 TAGCTGGGTTCTGTATTTCACTTCTTCGATACCGCTTAGGGTAAATGTCACTACAGAAA 1555  
Qy 1320 AAACTGTCAAGTGAGACACCTGATTCGGTTCCTTAACTTAAAGCTCCATGTCC 1379  
Db 1556 AAACTGTCAAGTGAGACACCTGATTCGGTTCCTTAACTTAAAGCTCCATGTCC 1615  
Qy 1380 TGGGCTTAAATCGTATAAATCTGGA-TTTTTTTTTTTTTTTTTTTTTGTCTCATTTACATA 1438  
Db 1616 TGGGCTTAAATCGTATAAATCTGGA-TTTTTTTTTTTTTTTTTTTTTGTCTCATTTACATA 1675  
Qy 1439 TGTAAACAGAACATCTATGATACATAAACTGGTTTTTAAAGGAACTATGTTGCTA 1498  
Db 1676 TGTAAACAGAACATCTATGATACATAAACTGGTTTTTAAAGGAACTATGTTGCTA 1735  
Qy 1499 TGAATTAACCTTGTCATGCTGATAGGA 1527  
Db 1736 TGAATTAACCTTGTCATGCTGATAGGA 1764

## RESULT 6

US-09-457-066-50  
; Sequence 50, Application US/09457066  
; Patent No. 6432673  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVBF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 50  
; LENGTH: 1095  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fused DNA  
US-09-457-066-50

Query Match 62.2%; Score 955.6; DB 4; Length 1095;  
Best Local Similarity 99.9%; Pred. No. 9.8e-259;  
Matches 955; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 GTAAATTCAGTTTCCAGCAACAGGAAACAGAGACGAGATCAAGATCTCTCAGCATGAGA 63  
Db 122 GTAAATTCAGTTTCCAGCAACAGGAAACAGAGACGAGATCAAGATCTCTCAGCATGAGA 181  
Qy 64 GAATTTATCTGTCTCTACTTAATGGAAGTATTCACAGCCCAAGGTTTCTCTCATCTTATC 123  
Db 182 GAATTTATCTGTCTCTACTTAATGGAAGTATTCACAGCCCAAGGTTTCTCTCATCTTATC 241  
Qy 124 CAAGAAATACCGTCTTGGTATGGAATTTAGTAGCAGTAGAGGAAATGTATGGATACAAC 183  
Db 242 CAAGAAATACCGTCTTGGTATGGAATTTAGTAGCAGTAGAGGAAATGTATGGATACAAC 301  
Qy 184 TTACGTTTGTATGAAGAATTTGGGCTTGAAGCCAGAGATGACATATGCAAGTATGATT 243  
Db 302 TTACGTTTGTATGAAGAATTTGGGCTTGAAGCCAGAGATGACATATGCAAGTATGATT 361  
Qy 244 TTGTAGAAGTTGAGGAACCCAGTGTGAACTATATTAGGGCGCTGGTGTGGTCTTGGTA 303  
Db 362 TTGTAGAAGTTGAGGAACCCAGTGTGAACTATATTAGGGCGCTGGTGTGGTCTTGGTA 421  
Qy 304 CTGTACCAAGAAAACAGATTTCTAAAGGAAATCAAAATTTAGGATAAGATTTGTATCTGATG 363  
Db 422 CTGTACCAAGAAAACAGATTTCTAAAGGAAATCAAAATTTAGGATAAGATTTGTATCTGATG 481  
Qy 364 AATATTTTCTCTCGAACCCAGGTTTTCGATCCACTACACATTTGTCATGCGCAATTTCA 423  
Db 482 AATATTTTCTCTCGAACCCAGGTTTTCGATCCACTACACATTTGTCATGCGCAATTTCA 541  
Qy 424 CAGAAGCTGTGAGTCTCTCAGTGTCTACCCCTTTCAGGCTTTGCCACTGGACCTGCTTAATA 483  
Db 542 CAGAAGCTGTGAGTCTCTCAGTGTCTACCCCTTTCAGGCTTTGCCACTGGACCTGCTTAATA 601  
Qy 484 ATGCTATACTGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTGAAACAGAGAT 543  
Db 602 ATGCTATACTGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTGAAACAGAGAT 661  
Qy 544 GGCAGTTGGACTTAGAGATCTATATAGGCCAACTTGGCACTTCTTGGCAAGCTTTTG 603  
Db 662 GGCAGTTGGACTTAGAGATCTATATAGGCCAACTTGGCACTTCTTGGCAAGCTTTTG 721  
Qy 604 TTTTGTGAAGAAATCCAGAGTGTGTGATCTGAACCTTCTAAACAGAGAGGTAAAGATTAT 663  
Db 722 TTTTGTGAAGAAATCCAGAGTGTGTGATCTGAACCTTCTAAACAGAGAGGTAAAGATTAT 781  
Qy 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 723  
Db 782 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 841  
Qy 724 CCATTTTCTGCCAGGTTTCTCCTCGTTTAAACCTGTGGTGGGAACCTGCTGTTGCTC 783  
Db 842 CCATTTTCTGCCAGGTTTCTCCTCGTTTAAACCTGTGGTGGGAACCTGCTGTTGCTC 901  
Qy 784 TCCACAAATTCGAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTTAAATAATACCAAGG 843  
Db 902 TCCACAAATTCGAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTTAAATAATACCAAGG 961  
Qy 844 TCCTTCAGTTGAGACCAAAACCCGTTGTAGGGGATTTGCAAAATCACTACCGACGTGG 903  
Db 962 TCCTTCAGTTGAGACCAAAACCCGTTGTAGGGGATTTGCAAAATCACTACCGACGTGG 1021  
Qy 904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGTAG 959  
Db 1022 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGTAG 1077

## RESULT 7

US-09-706-968-50  
; Sequence 50, Application US/09706968  
; Patent No. 6528050

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; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fused DNA
US-09-706-968-50

Query Match      62.2%; Score 955.6; DB 4; Length 1095;
Best Local Similarity 99.9%; Pred. No. 9.8e-259;
Matches 955; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4  GTAATTTCCAGTTTTCAGACCAACAGGACAGAGGATACAGATCCCTCAGCATGAGA 63
DB      122  GTAATTTCCAGTTTTCAGACCAACAGGACAGAGGATACAGATCCCTCAGCATGAGA 181

QY      64  GAATTTATTACTGTCTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATCTTATC 123
DB      182  GAATTTATTACTGTCTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATCTTATC 241

QY      124  CAAGAAATACGGTCTTGATGGAGATAGTAGCAGTAGAGGAAATGTATGGATACAC 183
DB      242  CAAGAAATACGGTCTTGATGGAGATAGTAGCAGTAGAGGAAATGTATGGATACAC 301

QY      184  TTACGTTTGATGAAGATTTCGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
DB      302  TTACGTTTGATGAAGATTTCGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 361

QY      244  TTGTAGAAGTTGAGGAACCCAGTAGTGAACTATATTAGGCGCTGGTGTGGTTCTGGTA 303
DB      362  TTGTAGAAGTTGAGGAACCCAGTAGTGAACTATATTAGGCGCTGGTGTGGTTCTGGTA 421

QY      304  CTGTACCAAGGAAACAGATTTCTAAAGGAATCAAATTTAGGATGAAGTTTCTATCTGATG 363
DB      422  CTGTACCAAGGAAACAGATTTCTAAAGGAATCAAATTTAGGATGAAGTTTCTATCTGATG 481

QY      364  AATATTTTCCCTCTGAAACAGGGTTCTGCATCCACTACAACTTGTCTATGCCACAATTC 423
DB      482  AATATTTTCCCTCTGAAACAGGGTTCTGCATCCACTACAACTTGTCTATGCCACAATTC 541

QY      424  CAGAAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCGCACTGCACTGCTTAATA 483
DB      542  CAGAAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCGCACTGCACTGCTTAATA 601

QY      484  ATGCTATTAACCTGCTTTAGTACCTTGGAGACCTTATTTCGATATCTTCAACCCAGAGAT 543
DB      602  ATGCTATTAACCTGCTTTAGTACCTTGGAGACCTTATTTCGATATCTTCAACCCAGAGAT 661

QY      544  GCGAGTTGCACTTAGAAGATCTATATAGGCCAACTTGGCACTTCTTGGCAAGGCTTTTG 603
DB      662  GCGAGTTGCACTTAGAAGATCTATATAGGCCAACTTGGCACTTCTTGGCAAGGCTTTTG 721

QY      604  TTTTGGAGAAATPCCAGAGTGGTGAATCTGAACCTTCTAACAGAGAGGTAAAGATTAT 663
DB      722  TTTTGGAGAAATPCCAGAGTGGTGAATCTGAACCTTCTAACAGAGAGGTAAAGATTAT 781

QY      664  ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGACCGATA 723
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DB      782  ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGAGAACTAAAGAGAACCGATA 841
QY      724  CCATTTTCTGSCCAGGTTGTCTCTCTGTTTAAACGCTGTGTGGGAACTGTGCGCTTGTGTC 783
DB      842  CCATTTTCTGSCCAGGTTGTCTCTCTGTTTAAACGCTGTGTGGGAACTGTGCGCTTGTGTC 901
QY      784  TCACAAATTCGAATGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCACGAGG 843
DB      902  TCACAAATTCGAATGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCACGAGG 961
QY      844  TCCTTCAGTTGAGACCAAAACACCGGTGTCAAGGGATTGCAAAATCACTCAACCGACGTGG 903
DB      962  TCCTTCAGTTGAGACCAAAACACCGGTGTCAAGGGATTGCAAAATCACTCAACCGACGTGG 1021
QY      904  CCCTGGAGCACCAATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGATAG 959
DB      1022  CCCTGGAGCACCAATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGATAG 1077

RESULT 8
US-09-564-595D-34
; Sequence 34, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-09-564-595D-34

Query Match      46.9%; Score 721; DB 4; Length 3571;
Best Local Similarity 83.6%; Pred. No. 1.4e-192;
Matches 817; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY      4  GTAATTTCCAGTTTTCAGACCAACAGGAAACAGAGGATGACAGATCCTCAGCATGAGA 63
DB      1131  GCAAGTTCCAGCTCTCCAGCGACAGAGAACAGAGGATGAGATCCCGCATGAGA 1190

QY      64  GAATTTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATATCTTATC 123
DB      1191  GAGTTGTCACTATATCTGTTAATGGAGCATCCACAGCCCGAAGTTTCTCATATACATACC 1250

QY      124  CAAGAAATACGGTCTTGATGGAGATAGTAGCAGTAGAGGAAATGTATGGATACAC 183
DB      1251  CAAGAAATATGGTGTGCTGGTGTGGAGATTAGTTGCAAGTAGAGTGAATAATGTGCGGATCCAGC 1310

QY      184  TTACGTTTGATGAAGATTTCGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
DB      1311  TGACATTTGATGAGGATTTGGCTTGAAGATCCAGAGACGATATATGCAAGTATGATT 1370

QY      244  TTGTAGAAGTTGAGGAACCCAGTAGTGATGGAACCTATATTAGGGCGCTGGTGTGGTTCTGTA 303
DB      1371  TTGTAGAAGTTGAGGAGCCAGTAGTGATGGAAGTGTGTTTATAGGACGCTGGTGTGGTTCTGGA 1430
```

304 CTGTACAGGAAACAGATTTCTAAAGAAATCAAATTAGGATAGATTTGTATCTGATG 363  
1431 CTGTCCAGGAAACAGATTTCTAAAGAAATCAAATTAGGATAGATTTGTATCTGATG 1490  
364 AATATTTTCTTGAACAGGGTCTGCATCCACTACAAATTTGTGATGCAAAATCA 423  
1491 AGTATTTTCCATCTGAACCCGGATTTCTGCATCCACTACAGTATTTATCATGCAAGTCA 1550  
424 CAGAGCTGTGAGTCTTCAAGAGTCTGATCCCTTCAAGAGTCTTCAAGAGTCTTCAAG 483  
1551 CAGAAACACAGTCTTCAAGAGTCTGATCCCTTCAAGAGTCTTCAAGAGTCTTCAAG 1610  
484 ATGCTATAATGCTCTTCAAGAGTCTGATCCCTTCAAGAGTCTTCAAGAGTCTTCAAG 543  
1611 ATGCTGTGAGTCTTCAAGAGTCTGATCCCTTCAAGAGTCTTCAAGAGTCTTCAAG 1670  
544 GGCAGTGTGAGTCTTCAAGAGTCTGATCCCTTCAAGAGTCTTCAAGAGTCTTCAAG 603  
1671 GGCAGTGTGAGTCTTCAAGAGTCTGATCCCTTCAAGAGTCTTCAAGAGTCTTCAAG 1730  
604 TTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTCAAGAGTCTTCAAGAGTCTTCAAG 663  
1731 TGTATGGAGAAATCCAGAGTGTGGATCTGAACCTTCAAGAGTCTTCAAGAGTCTTCAAG 1790  
664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATA 723  
1791 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACAGATA 1850  
724 CAATTTCTGCGCAGGTTGTCTCTGTTAAAGCTGTGTGGAGTCTGTCCTGTTGTC 783  
1851 CCATTTCTGCGCAGGTTGTCTCTGTTAAAGCTGTGTGGAGTCTGTCCTGTTGTC 1910  
784 TCCCAATTTGCAATGAATGTCAATGTCTCAGTGTCCATAGGGAAGAACTAAAGAGAAC 843  
1911 TCCCAATTTGCAATGAATGTCAATGTCTCAGTGTCCATAGGGAAGAACTAAAGAGAAC 1970  
844 TCCCTCAGTGTGAGTCTTCAAGAGTCTGATCCCTTCAAGAGTCTTCAAGAGTCTTCAAG 903  
1971 TCCCTCAGTGTGAGTCTTCAAGAGTCTGATCCCTTCAAGAGTCTTCAAGAGTCTTCAAG 2030  
904 CCCTGGACACCATGAGGAGTGTGACTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 963  
2031 CTCTGGAAACACCAAGGAGTGTGACTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2090  
964 ATCACCACCAAGCTC 980  
2091 AGCCTTCTGAGCAGCAC 2107

## RESULT 9

US-09-706-968-42  
; Sequence 42, Application US/09706968  
; Patent No 6528050

## GENERAL INFORMATION:

; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/706,968  
; CURRENT FILING DATE: 2000-11-06  
; PRIOR APPLICATION NUMBER: US/09/541,752  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 42

; LENGTH: 3571

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:  
; NAME/KEY: CDS

; LOCATION: (1049) ... (2086)  
US-09-706-968-42

Query Match 46.9%; Score 721; DB 4; Length 3571;

Best Local Similarity 83.6%; Pred. No. 1.4e-192;

Matches 817; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 4 GTAAATTTCCAGTTTCCAGCAACAAGGAACAGACGAGTACAGATCCTCAGCATGAGA 63  
DB 1131 GCAAAGTTGCAAGCTCTCCAGCGACAGGAACAGACGAGTGCAGATCCCAGCATGAGA 1190  
QY 64 GAAATTTTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATACTTATC 123  
DB 1191 GAGTTGTCACTATATCTGTAATGGAGCATCCACAGCCCGAAGTTTCTCATATACATACC 1250  
QY 124 CAAGAAATACCGTCTTGGTATGGAGATTTAGTAGCAGTAGAGGAAATGTATGGATACAA 183  
DB 1251 CAAGAAATATCGTGTGTGGAGATTTAGTTGCAGTAGATGAAATGTGGGATCCAGC 1310  
QY 184 TTAGCTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243  
DB 1311 TGACATTTGATGAGAGATTTGGGCTTGAAGATCCAGAGACGATATATGCAAGTATGATT 1370  
QY 244 TTGTAGAAAGTTGAGGAACCCAGATGATGGAACCTATATTAGGGCGCTGGTGTGTTCTG 303  
DB 1371 TTGTAGAAAGTTGAGGAGCCAGATGATGGAAGTGTGTTAGGACGCTGGTGTGTTCT 1430  
QY 304 CTGTACCAAGGAAACAGATTTCTAAAGGAATCAAATTAGGATAGATTTGTATCTGATG 363  
DB 1431 CTGTGCCAGGAAAGCAGACTTCTTAAGGAAATCATATCAGGATAAGATTTGTATCTGATG 1490  
QY 364 AATATTTTCTTCTGAACACAGGTTCTGCATCCACTACAAATTTGTATGCCACATTTCA 423  
DB 1491 AGTATTTTCCATCTGAACCCGGATTTCTGCATCCACTACAGTATTTATCATGCAAGTCA 1550  
QY 424 CAGAACTGTGAGTCTTCAAGTGTACCCCTTCAAGTGTGCGACTGGACCTGTCTTAATA 483  
DB 1551 CAGAAACACAGTCTTCAAGTGTGCGCTTCAATTTGTCAATGGACCTGTCTCAACA 1610  
QY 484 ATGCTATAATGCTCTTCAAGTGTGCGCTTCAAGTGTGCGACTGGACCTGTCTTAATA 543  
DB 1611 ATGCTGTGAGTCTTCAAGTGTGCGCTTCAAGTGTGCGACTGGACCTGTCTTAATA 1670  
QY 544 GGCAGTGTGAGTCTTCAAGTGTGCGCTTCAAGTGTGCGACTGGACCTGTCTTAATA 603  
DB 1671 GGCAGTGTGAGTCTTCAAGTGTGCGCTTCAAGTGTGCGACTGGACCTGTCTTAATA 1730  
QY 604 TTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTCAAGAGGAGGTAAGATTAT 663  
DB 1731 TGTATGGAGAAATCCAGAGTGTGGATCTGAACCTTCAAGAGGAGGTAAGATTAT 1790  
QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATA 723  
DB 1791 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACAGATA 1850  
QY 724 CAATTTCTGCGCAGGTTGTCTCTGTTAAAGCTGTGTGGAGTCTGTCCTGTTGTC 783  
DB 1851 CCATTTCTGCGCAGGTTGTCTCTGTTAAAGCTGTGTGGAGTCTGTCCTGTTGTC 1910  
QY 784 TCCCAATTTGCAATGAATGTCAATGTCTCAGTGTCCATAGGGAAGAACTAAAGAGAAC 843  
DB 1911 TCCCAATTTGCAATGAATGTCAATGTCTCAGTGTCCATAGGGAAGAACTAAAGAGAAC 1970  
QY 844 TCCCTCAGTGTGAGTCTTCAAGAGTCTGATCCCTTCAAGAGTCTTCAAGAGTCTTCAAG 903  
DB 1971 TCCCTCAGTGTGAGTCTTCAAGAGTCTGATCCCTTCAAGAGTCTTCAAGAGTCTTCAAG 2030  
QY 904 CCCTGGACACCATGAGGAGTGTGACTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 963  
DB 2031 CTCTGGAAACACCAAGGAGTGTGACTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2090

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QY 964 ATCACCACGAGCAGCTC 980
Db 2091 AGCCTTCGTAGCAGCAC 2107

RESULT 10
US-09-457-066-42
; Sequence 42, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-09-457-066-42

Query Match 46.9%; Score 721; DB 4; Length 3573;
Best Local Similarity 83.6%; Pred. No. 1.4e-192;
Matches 817; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 4 GTAAATTCAGTTTCCAGCAGACGAGACGAGACGAGATCCCTCAGCATGAGA 63
Db 1131 GCAAGTTTGCAGCTCTCCAGCAGACGAGACGAGATCCCGGATGAGA 1190
QY 64 GAATATTACTGTCTTACTTAATCGAAGTATTACAGCCCAAGGTTTCTCATACTTATC 123
Db 1191 GAGTTGTCATATATCTGTGTAATGGAGATCCACAGCCCGAAGTTTCTCATCATACC 1250
QY 124 CAAGAAATACGCTTCTGATGAGATTTAGTAGCAGTAGAGAGAAATGATGAGATAAC 183
Db 1251 CAAGAAATATGTCGTGTGGAGATTAGTTGAGTAGATGAAATGTGGGATCCAGC 1310
QY 184 TTACGTTTGTAGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
Db 1311 TGACATTTGATGAGAGATTTGGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATT 1370
QY 244 TTGTAGAAGTTGAGAAACCCAGTGTATGAACTATATTAGGCGCTGGTGTGGTCTGTGTA 303
Db 1371 TTGTAGAAGTTGAGAGCCCAAGTGTGAACTGTTTAGGACGCTGGTGTGGTCTGGGA 1430
QY 304 CTGTACCAGGAAACAGATTTCTAAAGAAATCAAAATPAGGATAAGATTTGTATCTGATG 363
Db 1431 CTGTGCCAGGAAACAGACATTTCTAAAGAAATCATATCAGGATAAGATTTGTATCTGATG 1490
QY 364 AATATTTTCTCTGACACAGGTTCTGCATCCATCAACATTTGATGACCAATCA 423
Db 1491 AGTATTTTCCATCTGAAACCCGGAATTCGATCCCACTACAGTATTATATGACCAAGTCA 1550
QY 424 CAGAGCTGTGAGTCTTTCAGTGTGTACCCCTTTCAGCTTTGCGACTGACCTGTTAATA 483
Db 1551 CAGAAACCAAGATTCCTTGGTGTGTGCCCCCTTATCTTTGTCATTTGAGCTGTCTCAACA 1610
QY 484 ATGCTATAACTGCTTTAGTACCTTTGGAAGACCTTTATTCGATATCTTGAACCAAGAGAT 543
Db 1611 ATGCTGTGACTGCTTTCAGTACCTTTGGAAGAGCTGATTCGGTACCTAGCAGCATGAT 1670
QY 544 GGCAGTTGGACTTAGAGATCTATATAGGCCCAACTTGGCAACTTCTGGCAAGGCTTTTG 603

Db 1671 GGCAGGTGGACTTGGACAGCCTCTACAAGCCAAACATGGCAGCTTTTGGGCAAGGCTTTCC 1730
QY 604 TTTTGGAGAGAAAATCCAGAGTGTGTGATCTGAACCTTTCTAAACAGAGAGAGGTAAGATTAT 663
Db 1731 TGTATGGGAAAAAAGCAAAAGTGGTGAATCTGAATCTCTCTCAAGGAAGAGGTAACCTCT 1790
QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAGAACTAAAGAGAACCGGATA 723
Db 1791 ACAGCTGCACACCCCGGAACCTTCTCAGTGTCCATAAGGAGAGCTAAAGAGGACAGATA 1850
QY 724 CCATTTTCTGGCAGGTTTCTCTCTGCTTAAACCTGTGGTGGGAACTGTCCCTGTTGTC 783
Db 1851 CCATATTTCTGGCCAGGTTTCTCTCTGCTCAAGCCCTGTGGAGGAATTTGTCCTGTTGTC 1910
QY 784 TCCCAATTCGAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCACGAGG 843
Db 1911 TCCATATTCGATGATGTCTCAGTGTGTCCCAAGTTACAAAAGTACCATGAGG 1970
QY 844 TCCCTCAGTTGAGACCAAAACCCGCTGTCTCAGGGGATTCGACAAATCTACCCGACGTGG 903
Db 1971 TCCCTCAGTTGAGACCAAAACCTGAGTCAAGGATTCGATAAGTCACTCACTGATGTGG 2030
QY 904 CCCTGGAGCACCATGAGGAGTGTCTGCTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGC 963
Db 2031 CTCTGGAACACCACGAGGAATGTGACTGTGTGTAGAGGAACGCGAGGGTAACTGTC 2090
QY 964 ATCACCACGAGCAGCTC 980
Db 2091 AGCCTTCGTAGCAGCAC 2107

RESULT 11
US-09-457-066-6
; Sequence 6, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence derived from SEQ ID NOS: 1 and
; OTHER INFORMATION: 2
; NAME/KEY: misc feature
; LOCATION: (1)-(1035)
; OTHER INFORMATION: n = A,T,C or G
US-09-457-066-6

Query Match 44.6%; Score 684.4; DB 4; Length 1035;
Best Local Similarity 57.5%; Pred. No. 1.5e-182;
Matches 547; Conservative 239; Mismatches 166; Indels 0; Gaps 0;

QY 4 GTAAATTCAGTTTCCAGCAGACGAGACGAGATCAAGATCTCTCAGCATGAGA 63
Db 83 SNAARTTYCARTTYVSNWNSNAAVAARGARCAAAVGGNGTNCARGAYCCNCARCAVGARM 142
QY 64 GAATATTACTGTCTTACTTAATCGAAGTATTACAGCCCAAGGTTTCTCTATCTATC 123
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Db 143 GNATHATHACNGTWSNACNAAYGNGWSNATHCAYWSNCCNMGNTTCCNAYACNTAYC 202
Qy 124 CAAGAATACGGTCTTGATGAGATTAAGTACAGTAGAGGAAATGATGATGATCAAC 183
Db 203 CNMGNAAACNGTNYTNGTNGMNGTNGTNGCNGTNGGARGAAYTNGTNGATHCARY 262
Qy 184 TTACGTTTGTATGAAGATTTGGGCTTGAAGACCAGAGATGACATATGCAAGTATGATT 243
Db 263 TNACNTTGTGAGMNTTGGNTNGARGAYCNGARGAYGAVATHTGVAARTAYGAT 322
Qy 244 TTGTAGAGTTGAGAACACCGAGTGAATCTATATAGGGCGCTGGTGGTCTGGTA 303
Db 323 TYGTNGARTNGARGACCNWSNGAGVGNACNATHYTNNGMNGTGGTGYGWSNGNA 382
Qy 304 CTGTACAGAAACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTTGTATCTGATG 363
Db 383 CNGTNCNGNAAACARATHWSNARGNAAACARATHMGNATHMGNNTTGTGWSNGAYG 442
Qy 364 AATATTTTCTCTGAACACCGGTTCTGATCCACTCAACATTTGTCATGCCCAATTC 423
Db 443 ARTAYTTCCNWSNGARCCNGGNTTGTGATCAATTAATGATTAATGATTAAT 502
Qy 424 CAGAGCTGTGAGTCTTCTAGTCTACCCCTTCAGCTTTGCCACTGGACCTGTTAATA 483
Db 503 CNGARGCNGTWSNCCNWSNGTNYTNCNCCNWSNGTNYTNCNCTNGAYTTTNAAYA 562
Qy 484 ATGTATAACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACACGAGAT 543
Db 563 AYGCNATHACNGNTTWSNACNYTNGARGAYTNGATHTMGNATYTNNGARCCNGARMGNT 622
Qy 544 GGCAGTTTGGACTTAGAAGATCTATATAGGCAACTTGGCAACTTCTTGGCAAGCTTTTG 603
Db 623 GGCARYTNGAYTNGARGAYTNTAYMGNCCNACNTGGCARYTNYTNGNAAARGCNTTYG 682
Qy 604 TTTTGAAGAAATCCAGAGTGTGATCTGACCTTCTAAGACGAGGAGTAAATGAT 663
Db 683 TNYTNGNAAARGSNMNGTNGTNGAYTNTAYMGNCCNACNTGGCARYTNYTNGNAAARGCNTTYG 742
Qy 724 CCATTTCTGCCAGGTTGCTCCTGTTAAACGCTGTGGTGGAACTGTGGCTGTGTC 783
Db 803 CNAHTTCTGCCGNGTGYTNTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNG 862
Qy 784 TCCACATTCGATGATGATCAATGCTCCCAAGCAAGTACTAAGAAATACACGAGG 843
Db 863 TNCAYAAATGYAAGTGTGARTGTGCTGCTCCCAAGCAAGTACTAAGAAATACACGAGG 922
Qy 844 TCCTTCAGTTGAGACCAAAACCGGTTGTCAGGGGATGTCACAAATCACTCACCGACG 903
Db 923 TNYTNCARYTNGMGNCCNAAACNGGNTNGMGNNGTNGMGNNGTNGMGNNGTNGMGNNG 982
Qy 904 CCTGTGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGAGGACACAGGAGG 955
Db 983 CNYTNGARCAAYCAYGARGARTGTGAYTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1034
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## RESULT 12

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US-09-706-968-6
; Sequence 6, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF3
; FILE REFERENCE: 98-60C1
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; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence derived from SEQ ID NOS: 1 and
; OTHER INFORMATION: 2
; NAME/KEY: misc feature
; LOCATION: (1)...(1035)
; OTHER INFORMATION: n = A, T, C or G
; US-09-706-968-6
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Query Match 44.6%; Score 684.4; DB 4; Length 1035;
Best Local Similarity 57.5%; Pred. No. 1.5e-182;
Matches 547; Conservative 239; Mismatches 166; Indels 0; Gaps 0;
```

```
Qy 4 GTAAATCCAGTTTCCAGCAACAGGAACAGAACCGAGTACAAAGATCCCTCAGCATCAGA 63
Db 83 SNAARTTTCARTTYSNWSNAAAYAAARGARCARAAYGNGTNCARGAYCCNRCARCAARM 142
Qy 64 GAATATTTACTGTGTCTACTAATGGAAGATTTACAGCCCAAGGTTTCTCTCATATCTATC 123
Db 143 GNATHATHACNGTWSNACNAAAYGNGWSNATHCAYWSNCCNMGNTTCCNAYACNTAYC 202
Qy 124 CAAGAATACGGTCTTGTATGAGATTTAGTACAGTAGAGGAAATGATGATGATCAAC 183
Db 203 CNMGNAAACNGTNYTNGTNGMNGTNGTNGCNGTNGGARGAAYTNGTNGATHCARY 262
Qy 184 TTACGTTTGTATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGAT 243
Db 263 TNACNTTGTGAGMNTTGGNTNGARGAYCNGARGAYGATHTGVAARTAYGAT 322
Qy 244 TTGTAGAGTTGAGAACACCGAGTGAATCTATATAGGGCGCTGGTGGTCTGGTA 303
Db 323 TYGTNGARTNGARGACCNWSNGAGVGNACNATHYTNNGMNGTGGTGYGWSNGNA 382
Qy 304 CTGTACAGAAACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTTGTATCTGATG 363
Db 383 CNGTNCNGNAAACARATHWSNARGNAAACARATHMGNATHMGNNTTGTGWSNGAYG 442
Qy 364 AATATTTTCTCTGAAGACCTTCTAAGACGAGGATGACATATGCAAGTACTCAACATTC 423
Db 443 ARTAYTTCCNWSNGARCCNGGNTTGTGATCAATTAATGATTAATGATTAAT 502
Qy 424 CAGAGCTGTGAGTCTTCTAGTCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATA 483
Db 503 CNGARGCNGTWSNCCNWSNGTNYTNCNCCNWSNGTNYTNCNCTNGAYTTTNAAYA 562
Qy 484 ATGTATAACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACACGAGAT 543
Db 563 AYGCNATHACNGNTTWSNACNYTNGARGAYTNGATHTMGNATYTNNGARCCNGARMGNT 622
Qy 544 GGCAGTTTGGACTTAGAAGATCTATATAGGCAACTTGGCAACTTCTTGGCAAGCTTTTG 603
Db 623 GGCARYTNGAYTNGARGAYTNTAYMGNCCNACNTGGCARYTNYTNGNAAARGCNTTYG 682
Qy 604 TTTTGAAGAAATCCAGAGTGTGATCTGACCTTCTAAGACGAGGAGTAAATGAT 663
Db 683 TNYTNGNAAARGSNMNGTNGTNGAYTNTAYMGNCCNACNTGGCARYTNYTNGNAAARGCNTTYG 742
Qy 724 CCATTTCTGCCAGGTTGCTCCTGTTAAACGCTGTGGTGGAACTGTGGCTGTGTC 783
Db 803 CNAHTTCTGCCGNGTGYTNTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNG 862
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QY 54 CAGCATGAGAAATATTACTGTCTACTAATGGAAGTATTACAGCCCAAGTTTCCT 113
DB 243 CAGAGAGAGAGAAACATTCAGGTGACAGCAATGGCCATGTGAGAGTCTCGCTCCCG 302
QY 114 CATACTTATCCAGAAATACGGTCTTGGTATGAGATTAGTACGACGTAGAGGAAATGTA 173
DB 303 AACAGTACCCAGGAACTGCTTCTGACATGCTGGCTCCGTTTC---CCAGGAGAAACA 359
QY 174 TGGATACAACTTACGTTTGATGAAAGTTTGGCTTGAAGCCCAAGATGACATATGC 233
DB 360 CGGATACAACTGTCTTTCACCATCAATTCCGACTAGAGGAAACGAAATGACATTTGT 419
QY 234 AGTATGATTTGTAGAAAGTTGAGAACCCAGTGTGAA---CTATATTAGGGCGC 287
DB 420 AGGTATGATCTTGTGAAAGTTGAGAACTCTCAGAGAGCAGCACTGTGTGAGAGGAGA 479
QY 288 TGGTGTGCTTCTGCTACTGTACCAAGGAAACAGATTTCTAAAGGAAATCAAAATAGGATA 347
DB 480 TGGTGTGCCACAGGAGATCCCTCCAGGATACGTCAGAACCAACAGATTTAAATC 539
QY 348 AGATTTGATCTGATGAATATTTTCTTCTGAAACAGGGTTCTGCATCCACTACAAATT 407
DB 540 ACATTTAAGTCTGATGACTACTTTGTGCAAAACCTGGATTCAGATTTATTTCAATT 599
QY 408 GT----CATGCCAAATTCAGAGGTGTGAGTCTTCACTGTCTACCCCTTCAGCTTT 463
DB 600 GTGGAAGATTTCCAAACCGGAGAGCGCTCAGAGACCAACTGGGAATCAGTCACAGCTCT 659
QY 464 GCCACTGCACCTGCTTA----- 480
DB 660 TTCTCTGGGGTGTCTTATCACTCTCCATCAATACGGACCCCACTCTCACTGCTGATGCC 719
QY 481 ----ATAATGCTATAA CTGCCCTTTAGTACCTTGGAGAACCTTATTCGTATCTTGAACCA 536
DB 720 CTGGACAAAACGTGCGAGAAATTCGATACCGCTGGAAGATCTTACTTAAGCACTTCAATCCA 779
QY 537 GAGAGATGGCAGTTGGACTTAGAGATCTATATAGGCCCACTTGGCACTTCTTGGCAAG 596
DB 780 GTGTCTTGGCAAGATGATCTGGAGAAATTTGATCTGGACACCCCTCATATAGAGGAGG 839
QY 597 GCTTTTGTGTTTGGAGAAATTCAGAGTGTGTGATCTGAAACCTTCTTAACAGAGAGGATA 656
DB 840 TCATACCATGATCGGA-----AGTCCAAAGTGGACCTGGACAGCTCAATGATGATGTC 893
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RESULT 15

US-09-564-595D-52

; Sequence 52, Application US/09564595D

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; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles B.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US 09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)...(1205)
; US-09-564-595D-52
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Query Match 7.6%; Score 117.4; DB 4; Length 1472;  
Best Local Similarity 50.8%; Pred. No. 3.4e-23;  
Matches 493; Conservative 1; Mismatches 402; Indels 75; Gaps 6;

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QY 174 TGGATACAACTTACGTTTGATGAAAGTTTGGCTTGAAGCCCAAGATGACATATGC 233
DB 360 CGGATACAACTGTCTTTCACCATCAATTCCGACTAGAGGAAACGAAATGACATTTGT 419
QY 234 AGTATGATTTGTAGAAAGTTGAGAACCCAGTGTGAA---CTATATTAGGGCGC 287
DB 420 AGGTATGATCTTGTGAAAGTTGAGAACTCTCAGAGAGCAGCACTGTGTGAGAGGAGA 479
QY 288 TGGTGTGCTTCTGCTACTGTACCAAGGAAACAGATTTCTAAAGGAAATCAAAATAGGATA 347
DB 480 TGGTGTGCCACAGGAGATCCCTCCAGGATACGTCAGAACCAACAGATTTAAATC 539
QY 348 AGATTTGATCTGATGAATATTTTCTTCTGAAACAGGGTTCTGCATCCACTACAAATT 407
DB 540 ACATTTAAGTCTGATGACTACTTTGTGCAAAACCTGGATTCAGATTTATTTCAATT 599
QY 408 GT----CATGCCAAATTCAGAGGTGTGAGTCTTCACTGTCTACCCCTTCAGCTTT 463
DB 600 GTGGAAGATTTCCAAACCGGAGAGCGCTCAGAGACCAACTGGGAATCAGTCACAGCTCT 659
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DB 660 TTCTCTGGGGTGTCTTATCACTCTCCATCAATACGGACCCCACTCTCACTGCTGATGCC 719
QY 481 ----ATAATGCTATAA CTGCCCTTTAGTACCTTGGAGAACCTTATTCGTATCTTGAACCA 536
DB 720 CTGGACAAAACGTGCGAGAAATTCGATACCGCTGGAAGATCTTACTTAAGCACTTCAATCCA 779
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DB 780 GTGTCTTGGCAAGATGATCTGGAGAAATTTGATCTGGACACCCCTCATATAGAGGAGG 839
QY 597 GCTTTTGTGTTTGGAGAAATTCAGAGTGTGTGATCTGAAACCTTCTTAACAGAGAGGATA 656
DB 840 TCATACCATGATCGGA-----AGTCCAAAGTGGACCTGGACAGCTCAATGATGATGTC 893
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Db      |||||
Qy 717 ACCGATACCAATTTCTGGCCAGGTTGTCCTCGTTAAACGCTGTGGTGGGAACTGTGCC 776
Db      |||||
Qy 954 ACCAATGCAGTCTTCTTCCACGATGCCCTCCTCGTGAGCGCTGTGGTGGCAACTGTGGT 1013
Db      |||||
Qy 777 TGTGTCTCCACAATTCGAATGAATGTCAATGTGTCCCAAGCAAAAGTTTACTTAAAAAATAC 836
Db      |||||
Qy 1014 TGCGAACCTGTCAACTGGAAGTCTCTGCACATGCAGCTCAGGGAAGACAGTCAAGAGTAT 1073
Db      |||||
Qy 837 CACGAGTCTCTTCAAGTTGAGACC-----AAASAACGGTGTGAGGGGATTCACAAA 887
Db      |||||
Qy 1074 CATGAGGTATTGAAGTTTGAGCCTGGACATTTCAAGAGAAGGGGCAAAAGCTTAAGATATG 1133
Db      |||||
Qy 888 TCACCTACCGACGTCGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGC 947
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Qy 1134 GCTCTTGTGTATCCAGCTGGATCATCATGAGCGATGTGACTGTATCTGCAGCTCAAGA 1193
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Qy 948 ACAGGAGGATA 958
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Qy 1194 CCACCTCGATA 1204
Db      |||||
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Job time : 81.0293 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 03:42:52 ; Search time 378.148 Seconds  
(without alignments)  
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Perfect score: 1536  
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1532.6	99.8	2849	10	US-09-978-295A-487
5	1532.6	99.8	2849	10	US-09-978-697-487
6	1532.6	99.8	2849	10	US-09-978-192A-487
7	1532.6	99.8	2849	10	US-09-999-832A-487
8	1532.6	99.8	2849	11	US-09-978-189-487
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17	1532.6	99.8	2849	11	US-09-918-585A-487	Sequence 487, App
18	1532.6	99.8	2849	11	US-09-978-423A-487	Sequence 487, App
19	1532.6	99.8	2849	11	US-09-978-193A-487	Sequence 487, App
20	1532.6	99.8	2849	11	US-09-999-830A-487	Sequence 487, App
21	1532.6	99.8	2849	11	US-09-978-757A-487	Sequence 487, App
22	1532.6	99.8	2849	11	US-09-978-187B-487	Sequence 487, App
23	1532.6	99.8	2849	11	US-09-978-643A-487	Sequence 487, App
24	1532.6	99.8	2849	12	US-09-978-375A-487	Sequence 487, App
25	1532.6	99.8	2849	12	US-09-978-188A-487	Sequence 487, App
26	1532.6	99.8	2849	12	US-09-978-298A-487	Sequence 487, App
27	1532.6	99.8	2849	12	US-10-137-870-285	Sequence 285, App
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35	1532.6	99.8	2849	12	US-10-140-926-285	Sequence 285, App
36	1532.6	99.8	2849	12	US-10-141-698-285	Sequence 285, App
37	1532.6	99.8	2849	12	US-10-141-702-285	Sequence 285, App
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40	1532.6	99.8	2849	12	US-10-142-432-285	Sequence 285, App
41	1532.6	99.8	2849	12	US-10-142-767-285	Sequence 285, App
42	1532.6	99.8	2849	12	US-10-143-031A-487	Sequence 487, App
43	1532.6	99.8	2849	12	US-10-143-033-285	Sequence 285, App
44	1532.6	99.8	2849	12	US-10-144-994-285	Sequence 285, App
45	1532.6	99.8	2849	12	US-10-145-628-285	Sequence 285, App

ALIGNMENTS

RESULT 1

US-09-852-209A-4  
; Sequence 4, Application US/09852209A  
; Patent No. US20020164687A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/852,209A  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-852-209A-4  
Query Match 100.0%; Score 1535.6; DB 10; Length 1536;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	CGGGTAAATTCAGTTCCTGATTTTCCAGCAACAGAAACAGACGAGTACAGATCCTCAGCATG	60
Qy	61	AGAGAATTTACTGTGTCTTACTTAATGGAAGTATTCACAGCCCAAGGTTTCTCATACTT	120
Db	61	AGAGAATTTACTGTGTCTTACTTAATGGAAGTATTCACAGCCCAAGGTTTCTCATACTT	120
Qy	121	ATCCAGAAATACCGTCTTCGGTATGGAGATTTAGTAGCAGTAGAGGAAATGTATGGATAC	180
Db	121	ATCCAGAAATACCGTCTTCGGTATGGAGATTTAGTAGCAGTAGAGGAAATGTATGGATAC	180
Qy	181	AACCTAGCTTGTATGAAGATTTGGGCTTCAGAACCCAGAGATGACATATGCAAGTATG	240
Db	181	AACCTAGCTTGTATGAAGATTTGGGCTTCAGAACCCAGAGATGACATATGCAAGTATG	240
Qy	241	ATTTGTAGAGTTGAGAACCCAGTGTATTAAGGAAATCAAAATAGGATAAGATTTGTATCTG	300
Db	241	ATTTGTAGAGTTGAGAACCCAGTGTATTAAGGAAATCAAAATAGGATAAGATTTGTATCTG	300
Qy	301	GTACTGTACAGGAAACAGATTTCTAAGAAATCAAAATAGGATAAGATTTGTATCTG	360
Db	301	GTACTGTACAGGAAACAGATTTCTAAGAAATCAAAATAGGATAAGATTTGTATCTG	360
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Qy	421	TCACAGAGCTGTGAGTCTTCACTGTGTACCCCTTCAGCTTTGCCACTGCGACTGCTTA	480
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Qy	481	ATAATGCTATAACCTGCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACACAGA	540
Db	481	ATAATGCTATAACCTGCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACACAGA	540
Qy	541	GATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTGGCAAGGCTT	600
Db	541	GATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTGGCAAGGCTT	600
Qy	601	TTGTTTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGAGGTAAGAT	660
Db	601	TTGTTTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGAGGTAAGAT	660
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Db	781	GTCTCCCAATGCAATGAATGTCAATGTGTCCCAAGCAAGTTACTTAAATAATACCAAG	840
Qy	841	AGGTCTTTCAGTTCAGACCAAAACCCGCTGCAGGGATTCACAAATCACTCACCGACG	900
Db	841	AGGTCTTTCAGTTCAGACCAAAACCCGCTGCAGGGATTCACAAATCACTCACCGACG	900
Qy	901	TGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGCAGAGGGAGCACAGGAGATAGC	960
Db	901	TGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGCAGAGGGAGCACAGGAGATAGC	960
Qy	961	CGATATCACACAGAGCTTTGGCCAGAGCTGTGCAGTGCAGTGCAGTGCATTTATTAGA	1020
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Qy	1021	GAACGTATGCGTTATCTCCATCTTAACTCTCAGTTGTTTGGCTTCAAGGACCTTTCACTT	1080
Db	1021	GAACGTATGCGTTATCTCCATCTTAACTCTCAGTTGTTTGGCTTCAAGGACCTTTCACTT	1080

Qy	1081	CAGGATTTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACA	1140
Db	1081	CAGGATTTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACA	1140
Qy	1141	GCTCTTTTGAGAGAGGCGCTTAAAGGACAGAGAAAGGTCCTTCAATCGTGGAAAGAAAT	1200
Db	1141	GCTCTTTTGAGAGAGGCGCTTAAAGGACAGAGAAAGGTCCTTCAATCGTGGAAAGAAAT	1200
Qy	1201	TAAATGTTGTTAATAATAGATCACAGCTAGTTTTCAGATTTACCATGTACGTTTCCACT	1260
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Qy	1261	AGCTGGGTTCTGTATTTTCACTTCTTCGATACCGCTTAGGCTAATGTACGATACAGGAAA	1320
Db	1261	AGCTGGGTTCTGTATTTTCACTTCTTCGATACCGCTTAGGCTAATGTACGATACAGGAAA	1320
Qy	1321	AACTGTGCAAGTAGACACCTGATTCGTTGCCCTTAACTCTAAAGCTCCATGCTCT	1380
Db	1321	AACTGTGCAAGTAGACACCTGATTCGTTGCCCTTAACTCTAAAGCTCCATGCTCT	1380
Qy	1381	GGGCTTAAATTCGTATTAATCTGGATTTTCTTTTCTGCTCATATTCACATATG	1440
Db	1381	GGGCTTAAATTCGTATTAATCTGGATTTTCTTTTCTGCTCATATTCACATATG	1440
Qy	1441	TAAACCAAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATG	1500
Db	1441	TAAACCAAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATG	1500
Qy	1501	AATTAAACTTGTGTCTGATGCTGATAGGACAGACTGGA	1536
Db	1501	AATTAAACTTGTGTCTGATGCTGATAGGACAGACTGGA	1536

RESULT 2

US-10-131-600-4  
; Sequence 4, Application US/10131600  
; Publication No. US20030082670A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/10/131,600  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: US/09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/108,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1536  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-600-4

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Best Local Similarity		100.0%;	Pred. No. 0;		
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QY	61	AGAGATTTACTGTGTCTACTAATGGAAGATTCACAGCCCAAGTTTCCCTCATCTT	120		
DB	61	AGAGATTTACTGTGTCTACTAATGGAAGATTCACAGCCCAAGTTTCCCTCATCTT	120		
QY	121	ATCCAGAAATACGGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATGTATGATAC	180		
DB	121	ATCCAGAAATACGGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATGTATGATAC	180		
QY	181	AACCTAGCTTTGATGAAGAATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATG	240		
DB	181	AACCTAGCTTTGATGAAGAATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATG	240		
QY	241	ATTTGTAGAAATGAGAACCCAGTATGGAATCTATTTAGGGCGCTGGTGTGTTCTG	300		
DB	241	ATTTGTAGAAATGAGAACCCAGTATGGAATCTATTTAGGGCGCTGGTGTGTTCTG	300		
QY	301	GTACTGTACAGGAAACAGATTTCTAAAGGAAATCAAATTTAGGATAAGATTTGTATCTG	360		
DB	301	GTACTGTACAGGAAACAGATTTCTAAAGGAAATCAAATTTAGGATAAGATTTGTATCTG	360		
QY	361	ATGAATATTTTCTTGAACAGGGTTGTCATCCACTACAAATTTGTCATGCCAAT	420		
DB	361	ATGAATATTTTCTTGAACAGGGTTGTCATCCACTACAAATTTGTCATGCCAAT	420		
QY	421	TCACAGAGCTGTGAGTCTTCACTGTGTCACCCCTTCACTGTGTCACCTGCTT	480		
DB	421	TCACAGAGCTGTGAGTCTTCACTGTGTCACCCCTTCACTGTGTCACCTGCTT	480		
QY	481	ATAATGTATAAATCTGCTTTAGTACCTTTGGAAGACCTTTATTCGATATCTTGAACAGAGA	540		
DB	481	ATAATGTATAAATCTGCTTTAGTACCTTTGGAAGACCTTTATTCGATATCTTGAACAGAGA	540		
QY	541	GATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCACTTTTGGCAAGGCTT	600		
DB	541	GATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCACTTTTGGCAAGGCTT	600		
QY	601	TTGTTTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTACAGAGAGGTTAAGAT	660		
DB	601	TTGTTTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTACAGAGAGGTTAAGAT	660		
QY	661	TATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCG	720		
DB	661	TATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCG	720		
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DB	721	ATACATTTTCTGGCAGGTTGTCTCTGGTTTAAACGCTGTGGTGGAACTGTGCTGTT	780		
QY	781	GTCTCCAAATTTGCAATGCTCAATGTCTCCAGCAAGTACTTAAATAATACCAG	840		
DB	781	GTCTCCAAATTTGCAATGCTCAATGTCTCCAGCAAGTACTTAAATAATACCAG	840		
QY	841	AGGTCTCTCAGTTGAGACCAASACCGGTGTGAGGGGATTCACAAATCACTCACCGACG	900		
DB	841	AGGTCTCTCAGTTGAGACCAASACCGGTGTGAGGGGATTCACAAATCACTCACCGACG	900		
QY	901	TGGCCCTTGAGACCAATGAGGATGTGACTGTGTGTCAGAGGAGCACAGGAGGATAC	960		
DB	901	TGGCCCTTGAGACCAATGAGGATGTGACTGTGTGTCAGAGGAGCACAGGAGGATAC	960		
QY	961	CGCATCACCACAGAGCTCTTGGCCAGAGCTGTGAGTGCAGTGGCTGATCTATTAGA	1020		
DB	961	CGCATCACCACAGAGCTCTTGGCCAGAGCTGTGAGTGCAGTGGCTGATCTATTAGA	1020		
QY	1021	GAACGTATGCGTTATCTCCATCTTAATCTCAGTTGTGTTTCAAGGACCTTTTCATCTT	1080		

DB	1021	GAACGTATGCGTTATCTCCATCTTAATCTCAGTTGTTGCTTCAAGGACCTTTCACTT	1080		
QY	1081	CAGGATTTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTTAGGATTTGTGCAACA	1140		
DB	1081	CAGGATTTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTTAGGATTTGTGCAACA	1140		
QY	1141	GCTCTTTTGAGAGAGGCGCTTAAAGGACAGAGAAAGGCTTCAATCGTGAAGAAAT	1200		
DB	1141	GCTCTTTTGAGAGAGGCGCTTAAAGGACAGAGAAAGGCTTCAATCGTGAAGAAAT	1200		
QY	1201	TAAATGTTGTTAAATAGATCACAGCTAGTTTTCAGAGTTACCATGTACGTATTTCCACT	1260		
DB	1201	TAAATGTTGTTAAATAGATCACAGCTAGTTTTCAGAGTTACCATGTACGTATTTCCACT	1260		
QY	1261	AGCTGGGTTCTGTATTTTCACTTCTTTCGATACGCTTTAGGGTAAATGTCAAGTACAGGAAAA	1320		
DB	1261	AGCTGGGTTCTGTATTTTCACTTCTTTCGATACGCTTTAGGGTAAATGTCAAGTACAGGAAAA	1320		
QY	1321	AACTGTGCAAGTGAGCACCTGATTCGCTTCCCTTAACTCTAAAGCTCCATGCTCT	1380		
DB	1321	AACTGTGCAAGTGAGCACCTGATTCGCTTCCCTTAACTCTAAAGCTCCATGCTCT	1380		
QY	1381	GGGCTTAAATCGTATTAATCTGATTTTTTTTTTTTTTTTTTTTTTCTCATATTCACATATG	1440		
DB	1381	GGGCTTAAATCGTATTAATCTGATTTTTTTTTTTTTTTTTTTTTTCTCATATTCACATATG	1440		
QY	1441	TAAACCAAGACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATG	1500		
DB	1441	TAAACCAAGACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATG	1500		
QY	1501	AATTAACCTTGTGCTGATGCTGATAGGACAGACTGGA	1536		
DB	1501	AATTAACCTTGTGCTGATGCTGATAGGACAGACTGGA	1536		

RESULT 3  
US-10-178-442-1  
; Sequence 1, Application US/10178442  
; Publication No. US20030113870A1  
; GENERAL INFORMATION:  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Kuo, Sophia S.  
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1  
; FILE REFERENCE: 11669.112USD2  
; CURRENT APPLICATION NUMBER: US/10/178,442  
; CURRENT FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: US 09/265,686  
; PRIOR FILING DATE: 1999-03-10  
; PRIOR APPLICATION NUMBER: US 09/184,216  
; PRIOR FILING DATE: 1998-11-02  
; PRIOR APPLICATION NUMBER: US 09/040,220  
; PRIOR FILING DATE: 1998-03-17  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2825  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2689)..(2689)  
; OTHER INFORMATION: Any nucleotide  
US-10-178-442-1

Query Match 99.8%; Score 1532.6; DB 14; Length 2825;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GTAAATTCAGTTTCCAGCAACAGAGAAACAGAAACGAGTACAAAGTCTCAGCATGAGA 63  
DB 341 GTAAATTCAGTTTCCAGCAACAGAGAAACAGAAACGAGTACAAAGTCTCAGCATGAGA 400

QY	64	GAATTTACTGTCTCTACTATGGAAGTATTCACAGCCCAAGGTTTCCTCATCTATC	123
Db	401	GAATTTACTGTCTCTACTATGGAAGTATTCACAGCCCAAGGTTTCCTCATCTATC	460
QY	124	CAAGAATAACGGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATGTATGGATCAAC	183
Db	461	CAAGAATAACGGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATGTATGGATCAAC	520
QY	184	TTACGTTTGATGAAGAATTTGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT	243
Db	521	TTACGTTTGATGAAGAATTTGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT	580
QY	244	TTGTAGAGTTGAGAACCCAGGATGAACTATATAGGCGCTGGTGGTCTTGGTA	303
Db	581	TTGTAGAGTTGAGAACCCAGGATGAACTATATAGGCGCTGGTGGTCTTGGTA	640
QY	304	CTGTACCAAGAAACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTTGTATCTGATG	363
Db	641	CTGTACCAAGAAACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTTGTATCTGATG	700
QY	364	AATATTTTCTGTGAACCAAGGTTCTGCATCCACTACACATTTGTCACCAATTC	423
Db	701	AATATTTTCTGTGAACCAAGGTTCTGCATCCACTACACATTTGTCACCAATTC	760
QY	424	CAGAAGCTGTGAGTCTTCAAGTCTACCCCTTTCAGCTTTGCGCACTGACCTGTTAATA	483
Db	761	CAGAAGCTGTGAGTCTTCAAGTCTACCCCTTTCAGCTTTGCGCACTGACCTGTTAATA	820
QY	484	ATGCTATAACTGCTTCTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAAGAGAT	543
Db	821	ATGCTATAACTGCTTCTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAAGAGAT	880
QY	544	GGCAGTTGCACTTGAAGATCTATATAGGCACTTGGCACTTCTTGGCAAGGCTTTTG	603
Db	881	GGCAGTTGCACTTGAAGATCTATATAGGCACTTGGCACTTCTTGGCAAGGCTTTTG	940
QY	604	TTTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTTCTAACGAGAGGTAAGATTAT	663
Db	941	TTTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTTCTAACGAGAGGTAAGATTAT	1000
QY	664	ACAGTGCACACCTCGTAATCTTCAAGTGTCTCAAGGAGAACTAAAGAACCGATA	723
Db	1001	ACAGTGCACACCTCGTAATCTTCAAGTGTCTCAAGGAGAACTAAAGAACCGATA	1060
QY	724	CCATTTCTGCGCAGGTTGCTCCCTGTTTAAACGCTGTGGTGGAACTGTGCTGTGTC	783
Db	1061	CCATTTCTGCGCAGGTTGCTCCCTGTTTAAACGCTGTGGTGGAACTGTGCTGTGTC	1120
QY	784	TCCCAATTTGCAATGAATGTCAATGTGTCACCAAGAAAGTTTACTAAAAAATACCAAGG	843
Db	1121	TCCCAATTTGCAATGAATGTGTCACCAAGAAAGTTTACTAAAAAATACCAAGG	1180
QY	844	TCCTTCAGTTGAGCAAAACCGGTGTGAGGGATTCACAAATCACTCACCGAGG	903
Db	1181	TCCTTCAGTTGAGCAAAACCGGTGTGAGGGATTCACAAATCACTCACCGAGG	1240
QY	904	CCCTGAGCACCATGAGGAGTGTGATGTGTGTGAGAGGAGCAGAGGATGACCCG	963
Db	1241	CCCTGAGCACCATGAGGAGTGTGATGTGTGTGAGAGGAGCAGAGGATGACCCG	1300
QY	964	ATCACCAACAGCAGCTCTTGGCCAGAGCTGTGAGTGCAGTGGCTGATTTATAGAGAA	1023
Db	1301	ATCACCAACAGCAGCTCTTGGCCAGAGCTGTGAGTGCAGTGGCTGATTTATAGAGAA	1360
QY	1024	CGTATCGGTTATCTCATCTTAACTCTGAGTGTGCTTTCAGGACCTTTCATCTTCAG	1083
Db	1361	CGTATCGGTTATCTCATCTTAACTCTGAGTGTGCTTTCAGGACCTTTCATCTTCAG	1420
QY	1084	GATTTTACGTGCAATCTTGAAGAGGAGACATCAAAAGATTTAGGAGTTGTGCAACAGCT	1143
Db	1421	GATTTTACGTGCAATCTTGAAGAGGAGACATCAAAAGATTTAGGAGTTGTGCAACAGCT	1480
QY	1144	CTTTTGGAGGAGGCGCTTAAAGGACAGGAGAAAGGCTTTCATCTGTTGGAAGAAATTA	1203

RESULT 4

US-09-978-295A-487  
; Sequence 487, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gottard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavich, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13

1 PRIOR APPLICATION NUMBER: 60/066364  
2 PRIOR FILING DATE: 1997-11-21  
3 PRIOR APPLICATION NUMBER: 60/077450  
4 PRIOR FILING DATE: 1998-03-10  
5 PRIOR APPLICATION NUMBER: 60/077632  
6 PRIOR FILING DATE: 1998-03-11  
7 PRIOR APPLICATION NUMBER: 60/077641  
8 PRIOR FILING DATE: 1998-03-11  
9 PRIOR APPLICATION NUMBER: 60/077649  
10 PRIOR FILING DATE: 1998-03-11  
11 PRIOR APPLICATION NUMBER: 60/077791  
12 PRIOR FILING DATE: 1998-03-12  
13 PRIOR APPLICATION NUMBER: 60/078004  
14 PRIOR FILING DATE: 1998-03-13  
15 PRIOR APPLICATION NUMBER: 60/078886  
16 PRIOR FILING DATE: 1998-03-20  
17 PRIOR APPLICATION NUMBER: 60/078936  
18 PRIOR FILING DATE: 1998-03-20  
19 PRIOR APPLICATION NUMBER: 60/078910  
20 PRIOR FILING DATE: 1998-03-20  
21 PRIOR APPLICATION NUMBER: 60/078939  
22 PRIOR FILING DATE: 1998-03-20  
23 PRIOR APPLICATION NUMBER: 60/079294  
24 PRIOR FILING DATE: 1998-03-25  
25 PRIOR APPLICATION NUMBER: 60/079656  
26 PRIOR FILING DATE: 1998-03-26  
27 PRIOR APPLICATION NUMBER: 60/079664  
28 PRIOR FILING DATE: 1998-03-27  
29 PRIOR APPLICATION NUMBER: 60/079689  
30 PRIOR FILING DATE: 1998-03-27  
31 PRIOR APPLICATION NUMBER: 60/079663  
32 PRIOR FILING DATE: 1998-03-27  
33 PRIOR APPLICATION NUMBER: 60/079728  
34 PRIOR FILING DATE: 1998-03-27  
35 PRIOR APPLICATION NUMBER: 60/079786  
36 PRIOR FILING DATE: 1998-03-27  
37 PRIOR APPLICATION NUMBER: 60/079920  
38 PRIOR FILING DATE: 1998-03-30  
39 PRIOR APPLICATION NUMBER: 60/079923  
40 PRIOR FILING DATE: 1998-03-30  
41 PRIOR APPLICATION NUMBER: 60/080105  
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43 PRIOR APPLICATION NUMBER: 60/080107  
44 PRIOR FILING DATE: 1998-03-31  
45 PRIOR APPLICATION NUMBER: 60/080165  
46 PRIOR FILING DATE: 1998-03-31  
47 PRIOR APPLICATION NUMBER: 60/080194  
48 PRIOR FILING DATE: 1998-03-31  
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50 PRIOR FILING DATE: 1998-04-01  
51 PRIOR APPLICATION NUMBER: 60/080328  
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56 PRIOR FILING DATE: 1998-04-01  
57 PRIOR APPLICATION NUMBER: 60/081070  
58 PRIOR FILING DATE: 1998-04-08  
59 PRIOR APPLICATION NUMBER: 60/081049  
60 PRIOR FILING DATE: 1998-04-08  
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63 PRIOR APPLICATION NUMBER: 60/081195  
64 PRIOR FILING DATE: 1998-04-08  
65 PRIOR APPLICATION NUMBER: 60/081203  
66 PRIOR FILING DATE: 1998-04-09  
67 PRIOR APPLICATION NUMBER: 60/081229  
68 PRIOR FILING DATE: 1998-04-09  
69 PRIOR APPLICATION NUMBER: 60/081955  
70 PRIOR FILING DATE: 1998-04-15  
71 PRIOR APPLICATION NUMBER: 60/081817  
72 PRIOR FILING DATE: 1998-04-15  
73 PRIOR APPLICATION NUMBER: 60/081819

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75 PRIOR APPLICATION NUMBER: 60/081952  
76 PRIOR FILING DATE: 1998-04-15  
77 PRIOR APPLICATION NUMBER: 60/081838  
78 PRIOR FILING DATE: 1998-04-15  
79 PRIOR APPLICATION NUMBER: 60/082568  
80 PRIOR FILING DATE: 1998-04-21  
81 PRIOR APPLICATION NUMBER: 60/082569  
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83 PRIOR APPLICATION NUMBER: 60/082704  
84 PRIOR FILING DATE: 1998-04-22  
85 PRIOR APPLICATION NUMBER: 60/082804  
86 PRIOR FILING DATE: 1998-04-22  
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90 PRIOR FILING DATE: 1998-04-22  
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98 PRIOR FILING DATE: 1998-04-29  
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101 PRIOR APPLICATION NUMBER: 60/083496  
102 PRIOR FILING DATE: 1998-04-29  
103 PRIOR APPLICATION NUMBER: 60/083499  
104 PRIOR FILING DATE: 1998-04-29  
105 PRIOR APPLICATION NUMBER: 60/083545  
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109 PRIOR APPLICATION NUMBER: 60/083558  
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114 PRIOR FILING DATE: 1998-04-29  
115 PRIOR APPLICATION NUMBER: 60/083742  
116 PRIOR FILING DATE: 1998-04-30  
117 PRIOR APPLICATION NUMBER: 60/084366  
118 PRIOR FILING DATE: 1998-05-05  
119 PRIOR APPLICATION NUMBER: 60/084414  
120 PRIOR FILING DATE: 1998-05-06  
121 PRIOR APPLICATION NUMBER: 60/084441  
122 PRIOR FILING DATE: 1998-05-06  
123 PRIOR APPLICATION NUMBER: 60/084637  
124 PRIOR FILING DATE: 1998-05-07  
125 PRIOR APPLICATION NUMBER: 60/084639  
126 PRIOR FILING DATE: 1998-05-07  
127 PRIOR APPLICATION NUMBER: 60/084640  
128 PRIOR FILING DATE: 1998-05-07  
129 PRIOR APPLICATION NUMBER: 60/084598  
130 PRIOR FILING DATE: 1998-05-07  
131 PRIOR APPLICATION NUMBER: 60/084600  
132 PRIOR FILING DATE: 1998-05-07  
133 PRIOR APPLICATION NUMBER: 60/084627  
134 PRIOR FILING DATE: 1998-05-07  
135 PRIOR APPLICATION NUMBER: 60/084643  
136 PRIOR FILING DATE: 1998-05-07  
137 PRIOR APPLICATION NUMBER: 60/085339  
138 PRIOR FILING DATE: 1998-05-13  
139 PRIOR APPLICATION NUMBER: 60/085338  
140 PRIOR FILING DATE: 1998-05-13  
141 PRIOR APPLICATION NUMBER: 60/085323  
142 PRIOR FILING DATE: 1998-05-13  
143 PRIOR APPLICATION NUMBER: 60/085582  
144 PRIOR FILING DATE: 1998-05-15  
145 PRIOR APPLICATION NUMBER: 60/085700  
146 PRIOR FILING DATE: 1998-05-15

Query Match 99.8%; Score 1532.6; DB 10; Length 2849;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

4 GTAAATTCAGTTCAGGCAACAGGAACAGAGGAGTACAGATCCTCAGCATGAGA 63  
1267 TCCTTCAGTTGAGACCAAGACCCGGTGTCAAGGAGTTGCAAAATCACTCACCACGTGG 1266

367 GTAAATTCAGTTCAGGCAACAGGAACAGAGGAGTACAGATCCTCAGCATGAGA 426

64 GAATTTATCTGCTCTACTAATGMAAGTATTCAAGCCCAAGGTTTCTCATCTTATC 963  
904 CCTGGAGACCATGAGGAGTGTGACTGTGTGTGTCAGAGGAGACACAGGAGATAGCCGC 963

427 GAATTTATCTGCTCTACTAATGMAAGTATTCAAGCCCAAGGTTTCTCATCTTATC 486

1267 CCTGGAGACCATGAGGAGTGTGACTGTGTGTGTCAGAGGAGACACAGGAGATAGCCGC 1326

124 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 183

964 ATCACCAACGAGCTCTTCCAGAGCTGTGCCAGAGCTGTGCAGTGCAGTGGCTGATTTATTAGAGAA 1023

487 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 546

1327 ATCACCAACGAGCTCTTCCAGAGCTGTGCCAGAGCTGTGCAGTGCAGTGGCTGATTTATTAGAGAA 1386

184 TTAGCTTTGATGAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243

1024 GGTATGGTTTATCTCCATCTTAATCTCAGTTGTTTCTCAAGGACCTTTCATCTTCAG 1083

547 TTAGCTTTGATGAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 606

1387 GGTATGGTTTATCTCCATCTTAATCTCAGTTGTTTCTCAAGGACCTTTCATCTTCAG 1446

244 TTGTAGAGTTGAGGAACCCAGTGTGAACTATATTAGGGCGCTGGTGTCTCGTGA 303

1084 GATTTACAGTGCAATTCCTGAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCT 1143

607 TTGTAGAGTTGAGGAACCCAGTGTGAACTATATTAGGGCGCTGGTGTCTCGTGA 666

1447 GATTTACAGTGCAATTCCTGAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCT 1506

304 CTGTACCAAGGAAACAGATTTCTAAAGAAATCAAATTTAGGAGTATGATCTGATG 363

1144 CTTTTGAGAGGAGCCCTAAAGGACAGAGGAGGAGGTTCTTCAATCGTGGAAAGAAATTA 1203

667 CTGTACCAAGGAAACAGATTTCTAAAGAAATCAAATTTAGGAGTATGATCTGATG 726

1204 ATGTTGTATTAAATAGATCACCGCTAGTTTCAGAGTTACCATGTACGTATTCACACTAGC 1263

607 TTGTAGAGTTGAGGAACCCAGTGTGAACTATATTAGGGCGCTGGTGTCTCGTGA 666

1567 ATGTTGTATTAAATAGATCACCGCTAGTTTCAGAGTTACCATGTACGTATTCACACTAGC 1626

364 AATATTTTCTCTGAAACAGGTTCTGCATCCACTCAACATTTGTCATGCCAATTC 423

1264 TGGGTTCTGATTTTTCAGTTCTTTCGATACCGCTTAGGGTAAATGTCAGTACAGGAAAAA 1323

607 TTGTAGAGTTGAGGAACCCAGTGTGAACTATATTAGGGCGCTGGTGTCTCGTGA 666

1627 TGGGTTCTGATTTTTCAGTTCTTTCGATACCGCTTAGGGTAAATGTCAGTACAGGAAAAA 1686

304 CTGTACCAAGGAAACAGATTTCTAAAGAAATCAAATTTAGGAGTATGATCTGATG 363

1324 CTGTGCAAGTACAGACCTGATTCGTTGCGCTTGTCTTAACTCTAAAGTCCATGCTCGG 1383

607 TTGTAGAGTTGAGGAACCCAGTGTGAACTATATTAGGGCGCTGGTGTCTCGTGA 666

1687 CTGTGCAAGTACAGACCTGATTCGTTGCGCTTGTCTTAACTCTAAAGTCCATGCTCGG 1746

304 CTGTACCAAGGAAACAGATTTCTAAAGAAATCAAATTTAGGAGTATGATCTGATG 363

1384 CCTAAATTCGATATAAATCTCGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTAA 1443

607 TTGTAGAGTTGAGGAACCCAGTGTGAACTATATTAGGGCGCTGGTGTCTCGTGA 666

1747 CCTAAATTCGATATAAATCTCGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTAA 1806

1444 ACCGAAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1503

1807 ACCGAAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1866

1504 TAAACTTGTGCTGCTCATGATAGGACAGACTGGA 1536

1867 TAAACTTGTGCTGCTCATGATAGGACAGACTGGA 1899

RESULT 5  
US-09-978-697-487  
Sequence 487, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;



APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C27  
CURRENT APPLICATION NUMBER: US/09/978,697  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
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PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
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PRIOR FILING DATE: 1998-03-30  
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PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
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DB	487	CAAGAAATACGTTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC	546						
QY	184	TTACGTTTGTATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT	243						
DB	547	TTACGTTTGTATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT	606						
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QY	304	CTGTACAGGAAACAGATTTCTAAGGAAATCAAAATTAGGATAGATTTGTATCTGATG	363						
DB	667	CTGTACAGGAAACAGATTTCTAAGGAAATCAAAATTAGGATAGATTTGTATCTGATG	726						
QY	364	AATATTTTCTTCTGAACAGGGTTCTGCATCCACTACAAATTTGTATGCCACAATTC	423						
DB	727	AATATTTTCTTCTGAACAGGGTTCTGCATCCACTACAAATTTGTATGCCACAATTC	786						
QY	424	CAGAGCTGTGAGTCTTCTGAGTGTACCCCTTCTGAGTTTCCCACTGAGCTGTCTTAATA	483						
DB	787	CAGAGCTGTGAGTCTTCTGAGTGTACCCCTTCTGAGTTTCCCACTGAGCTGTCTTAATA	846						
QY	484	ATGCTATAACTGCCTTTAGTACTTGGAGACCTTTATTCGATATCTTTGAACAGAGAT	543						
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QY	844	TCCTTCAGTTGAGACCAAAACCGGTGTCCAGGGGATTGCAAAATCACTCACCAGCTGG	903
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QY	904	CCCTGGAGCCATGAGGAGTGTGACTGTGTGCAGAGGGAGACACAGGAGGATAGCCGC	963
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; APPLICANT: Ashkenazi, Avi  
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Db 1747 CCTAAATCGTATAAAATCTGGATTTTCTGCTCATATTCACATATGTA 1806
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Db 1807 ACCGAACATCTATGTACTACAAACCTGGTTTTTAAAGGAATATGTTGCTATGAAT 1866
Qy 1504 TAACTTGTGTCATGCTGATAGGACAGACTGGA 1536
Db 1867 TAACTTGTGTCATGCTGATAGGACAGACTGGA 1899

RESULT 7
US-09-999-832A-487
; Sequence 487, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: ROY, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
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## RESULT 8

US-09-978-189-487  
; Sequence 487, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
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; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C7  
; CURRENT APPLICATION NUMBER: US/09/978,189  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30  
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73	PRIOR APPLICATION NUMBER: 60/085338



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Db 1867 TAAACTTGTGATGCTGATAGGACAGACTGGA 1899
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RESULT 10

US-09-978-585A-487  
; Sequence 487, Application US/0997858A  
; Publication No. US20030049633A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi

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; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deanoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C15  
; CURRENT APPLICATION NUMBER: US/09/978,585A  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 487  
; LENGTH: 2849  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: unsure  
; LOCATION: 2715  
; OTHER INFORMATION: unknown base  
US-09-978-585A-487
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Db 907 GCGAGTTGACCTTAGAAGATCTATAGCCAACTTGGCAACTTCTTGCGAAGGCTTTTG 966  
Qy 604 TTTTGGAAAGAAATCCAGAGTGTGATCTGAACCTTCTTAACAGAGGAGTGAATAT 663  
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; Sequence 487, Application US/09978191A  
; Publication No. US20030050239A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PLC4  
; CURRENT APPLICATION NUMBER: US/09/978,191A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.8%; Score 1532.6; DB 11; Length 2849;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 367 GTAAATTCAGTTTTCCAGCAACAGGAGTACAGATCCTCAGCATGAGA 426

QY 64 GAATATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTATATTTC 123

Db 427 GAATTATTACTGTCTACTAAATGAAGATTATCACAGCCCAAGGTTTCTCTATACCTTATC 486  
Qy 124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGATGGATACAAC 183  
Db 487 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGATGGATACAAC 546  
Qy 184 TTACGTTTGATGAAGAATTTGGCTTTGAAGACCCAGAAATGACATATGCAAGATGATT 243  
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## RESULT 12

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; Sequence 487, Application US/09978403A  
; Publication No. US20030050240A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
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; APPLICANT: Napier, Mary A.  
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; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C17  
; CURRENT APPLICATION NUMBER: US/09/978,403A  
; PRIOR FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: 09/918585  
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115 PRIOR APPLICATION NUMBER: 60/084366  
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126 PRIOR FILING DATE: 1998-05-07  
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141 PRIOR APPLICATION NUMBER: 60/085582  
142 PRIOR FILING DATE: 1998-05-15  
143 PRIOR APPLICATION NUMBER: 60/085700  
144 PRIOR FILING DATE: 1998-05-15  
145 PRIOR APPLICATION NUMBER: 60/085689  
146 PRIOR FILING DATE: 1998-05-15



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PRIOR APPLICATION NUMBER: 60/085697									
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Best Local Similarity 99.98; Pred. No. 0;									
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;									
Qy	4	GTAAATTCAGT	TTTCAGCAAAAGGAAAGGAGTACAGATCCTCAGCATGAGA	63					
Db	367	GTAAATTCAGT	TTTCAGCAAAAGGAAAGGAGTACAGATCCTCAGCATGAGA	426					
Qy	64	GAATATATCTGT	CTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATCTTATC	123					
Db	427	GAATATATCTGT	CTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATCTTATC	486					
Qy	124	CAAGAAATACGG	CTTCGGTATGGAGTATAGCAGTAGAGGAAATGTATGGATCAAC	183					
Db	487	CAAGAAATACGG	CTTCGGTATGGAGTATAGCAGTAGAGGAAATGTATGGATCAAC	546					
Qy	184	TTACGTTTGTAT	GAAAGTATGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGAT	243					
Db	547	TTACGTTTGTAT	GAAAGTATGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGAT	606					
Qy	244	TTGTAGAAGT	GTAGGAAACCCAGTATATATTTAGGGCGCTGGTGTCTGGTA	303					
Db	607	TTGTAGAAGT	GTAGGAAACCCAGTATATATTTAGGGCGCTGGTGTCTGGTA	666					
Qy	304	CTGTACAGAA	ACACATCTTCAAGGAAATCAATTTAGGATAGATTTGTATCTGATG	363					
Db	667	CTGTACAGAA	ACACATCTTCAAGGAAATCAATTTAGGATAGATTTGTATCTGATG	726					
Qy	364	AAATATTTCT	CTTGAAACCCAGGTTCTGCATCCACTACAACTGTATGCCACAAATCA	423					
Db	727	AAATATTTCT	CTTGAAACCCAGGTTCTGCATCCACTACAACTGTATGCCACAAATCA	786					
Qy	424	CAGAGCTGT	GAGTCCCTTCACTGTCACCCCTTCAGCTTTGCGCATGGAACCTGTTAATA	483					
Db	787	CAGAGCTGT	GAGTCCCTTCACTGTCACCCCTTCAGCTTTGCGCATGGAACCTGTTAATA	846					
Qy	484	ATGCTATACT	CGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCCAGAGAT	543					
Db	847	ATGCTATACT	CGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCCAGAGAT	906					
Qy	544	GGCAGTTGG	ACTTAGAAGTCTATATAGGCCAACTTGGCAACTCTTTGGCAAGCTTTTG	603					
Db	907	GGCAGTTGG	ACTTAGAAGTCTATATAGGCCAACTTGGCAACTCTTTGGCAAGCTTTTG	966					
Qy	604	TTTTTGAAGA	AAATCCAGAGTGTGATCTGACCTTCTAACAGAGAGTATAGATTAT	663					
Db	967	TTTTTGAAGA	AAATCCAGAGTGTGATCTGACCTTCTAACAGAGAGTATAGATTAT	1026					
Qy	664	ACAGCTGCA	CACTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA	723					
Db	1027	ACAGCTGCA	CACTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA	1086					
Qy	724	CAATTTTCT	CGCCAGGTGTCTCTCGTTAAACGCTGTGGGAACCTGTGCTGTGTC	783					
Db	1087	CAATTTTCT	CGCCAGGTGTCTCTCGTTAAACGCTGTGGGAACCTGTGCTGTGTC	1146					
Qy	784	TCCAAATTC	CAATGAATGCAATGTCTCCCAACCAAGTTACTAAAAATACCAAGG	843					
Db	1147	TCCAAATTC	CAATGAATGCAATGTCTCCCAACCAAGTTACTAAAAATACCAAGG	1206					
Qy	844	TCCTTTCA	GTGAGACCAACCGGTGTGAGGGGATTCGCAAAATCACTACCAAGCTGG	903					
Db	1207	TCCTTTCA	GTGAGACCAACCGGTGTGAGGGGATTCGCAAAATCACTACCAAGCTGG	1266					

Qy	904	CCCTGGAGCA	CCATGAGGAGTGTGACTGTGTGCAGAGGAGCACAGGATAGCCGC	963					
Db	1267	CCCTGGAGCA	CCATGAGGAGTGTGACTGTGTGCAGAGGAGCACAGGATAGCCGC	1326					
Qy	964	ATACACCA	CCAGCAGCTTTCGCCAGAGCTGTGCAGTGCAGTGGCTGATCTTATTAGAGAA	1023					
Db	1327	ATACACCA	CCAGCAGCTTTCGCCAGAGCTGTGCAGTGCAGTGGCTGATCTTATTAGAGAA	1386					
Qy	1024	CGTATGCT	TATCTCCATCTTAATCTCAGTTGTTTCTCAAGACCTTTCATCTTCAG	1083					
Db	1387	CGTATGCT	TATCTCCATCTTAATCTCAGTTGTTTCTCAAGACCTTTCATCTTCAG	1446					
Qy	1084	GATTTCAG	TGCATTTCTGAAGAGGAGACATCAAAACAGAAATTAGAGTTGTGCAACAGCT	1143					
Db	1447	GATTTCAG	TGCATTTCTGAAGAGGAGACATCAAAACAGAAATTAGAGTTGTGCAACAGCT	1506					
Qy	1144	CTTTTGAG	GAGGCGCTTAAAGACAGGAGAAAGGTTCTCAATCGTGGAAAGAAATTTAA	1203					
Db	1507	CTTTTGAG	GAGGCGCTTAAAGACAGGAGAAAGGTTCTCAATCGTGGAAAGAAATTTAA	1566					
Qy	1204	ATGTTGTA	TATAATAGATCACCGACTAGTTTCAGAGTTACCATGTACGTATTCACACTAGC	1263					
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RESULT 13

US-09-978-564A-487  
; Sequence 487, Application US/09978564A  
; Publication No. US20030050241A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC25  
CURRENT APPLICATION NUMBER: US/09/978,564A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.8%; Score 1532.6; DB 11; Length 2849;  
Best Local Similarity 99.9%; Pred. No. 0;  
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DB 367 GTAAATTCAGTTTCCAGCAACAAGGACAGAAAGGATACAGATCCCTCAGCATGAGA 426  
  
QY 64 GAATTAATTAAGTGTCTACTTAATGGAAGTATTCAGAGCCCAAGGTTTCTCATACTATC 123  
DB 427 GAATTAATTAAGTGTCTACTTAATGGAAGTATTCAGAGCCCAAGGTTTCTCATACTATC 486  
  
QY 124 CAAGAAATACGGTCTGGTATGAGATTAAGTATGAGGAAATGATGATGATCAAC 183  
DB 487 CAAGAAATACGGTCTGGTATGAGATTAAGTATGAGGAAATGATGATGATCAAC 546  
  
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DB 607 TTGTAGAGTTGAGGAACCCAGTGTAGGAACTATATATAGGGCGCTGGTGGTTCTGGTA 666  
  
QY 304 CTGTACCAAGAAACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTTGATCTGATG 363  
DB 667 CTGTACCAAGAAACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTTGATCTGATG 726  
  
QY 364 AATATTTTCTCTGAAACAGGGTTCTGATCCACTACAACTTGTATGTCACCAATTC 423  
DB 727 AATATTTTCTCTGAAACAGGGTTCTGATCCACTACAACTTGTATGTCACCAATTC 786  
  
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DB 1627 TGGGTTCTGTATTTCAAGTCTTTCGATACCGCTTAGGTAATGTCTCAGTACAGGAAAATA 1686  
  
QY 1324 CTGTCAAGTGTAGCAGCTGATTCCTGCTTCAACTCTAAAGCTCCATGTCCCTGGG 1383  
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QY 1384 CTTAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTTTTTTTTCCTCATATTCACATATGAA 1443  
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QY 1504 TAAACTTGTGTCAATGCTGATAGGACAGACTGGA 1536  
DB 1867 TAAACTTGTGTCAATGCTGATAGGACAGACTGGA 1899

RESULT 14  
US-09-999-833A-487  
; Sequence 487, Application US/09999833A  
; Publication No. US20030054405A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C65  
CURRENT APPLICATION NUMBER: US/09/999,833A  
CURRENT FILING DATE: 2001-10-24  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
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QY	484	ATGCTATATACTGCCTTTAGTACCTTGGAAAGACCTTATTCGATATCTTGAACACAGAGAT	543
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QY	784	TCCAAATTTGCAATGAATGTCAATGTCTCCAGCAAGAACTTACTAAATAATACACGAGG	843
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Search completed: November 26, 2003, 09:32:29  
Job time : 382.148 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 23:55:21 ; Search time 3278.48 Seconds  
(without alignments)  
15537.553 Million cell updates/sec

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Gapop 10.0, Gapext 1.0

Searched: 33363688 seqs, 1658189874 residues

Total number of hits satisfying chosen parameters: 66727376

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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2	1535.6	100.0	1536	2	PCT-US99-22668-4
3	1535.6	100.0	1536	21	US-09-410-349A-4
4	1535.6	100.0	1536	35	US-09-852-209-4

Sequence 4, Appli  
Sequence 4, Appli  
Sequence 4, Appli



961	Db	CGCATCACCA	CGAGAGCTCTGCCAGAGAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGA	1020
1021	Qy	GAACGATGCGT	TATCTCCATCTTAACTCAGTTGTTGCTTCAAGGACCTTTCATCTT	1080
1021	Db	GAACGATGCGT	TATCTCCATCTTAACTCAGTTGTTGCTTCAAGGACCTTTCATCTT	1080
1081	Qy	CAGGATTTAC	AGTGCATCTTGAAGAGGAGACATCAAAAGAAATTAGGAGTTGTGCAACA	1140
1081	Db	CAGGATTTAC	AGTGCATCTTGAAGAGGAGACATCAAAAGAAATTAGGAGTTGTGCAACA	1140
1141	Qy	GCTCTTTTGAG	GAGGAGCCTTAAGGACAGAGAAAGCTCTCAATCGTGGAAAGAAAT	1200
1141	Db	GCTCTTTTGAG	GAGGAGCCTTAAGGACAGAGAAAGCTCTCAATCGTGGAAAGAAAT	1200
1201	Qy	TAAATGTTGTA	TAAATAGATCACCACTAGTTTCAGAGTTACCATGATCGTATTCACAT	1260
1201	Db	TAAATGTTGTA	TAAATAGATCACCACTAGTTTCAGAGTTACCATGATCGTATTCACAT	1260
1261	Qy	AGCTGGGTTCT	GTATTTTCAGTTCTTTTCGATACCGCTTAGGGTAATGTCAGTACAGGAAA	1320
1261	Db	AGCTGGGTTCT	GTATTTTCAGTTCTTTTCGATACCGCTTAGGGTAATGTCAGTACAGGAAA	1320
1321	Qy	AAACTGTGCAAG	TAGGACACCTGATTCGCTTGCCTTGCTTAACTCTAAAGCTCCATGTCCT	1380
1321	Db	AAACTGTGCAAG	TAGGACACCTGATTCGCTTGCCTTGCTTAACTCTAAAGCTCCATGTCCT	1380
1381	Qy	GGGCTTAAAT	CTGATATAAATCTGGATTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATG	1440
1381	Db	GGGCTTAAAT	CTGATATAAATCTGGATTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATG	1440
1441	Qy	TAAACCAAGAC	ATTCTATGTACTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATG	1500
1441	Db	TAAACCAAGAC	ATTCTATGTACTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATG	1500
1501	Qy	AAATTAACCT	TGTGTGCTCATGCTGATAGGACAGACTGGA	1536
1501	Db	AAATTAACCT	TGTGTGCTCATGCTGATAGGACAGACTGGA	1536

RESULT 2					
PCT-US99-22668-4					
; Sequence 4, Application PC/TUS9922668B					
; GENERAL INFORMATION:					
; APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH					
; APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.					
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,					
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF					
; FILE REFERENCE: PCT/US99/22669-LUDWIG INST FOR CANCER					
; CURRENT APPLICATION NUMBER: PCT/US99/22668B					
; CURRENT FILING DATE: 1999-09-30					
; EARLIER APPLICATION NUMBER: 60/102,461					
; EARLIER FILING DATE: 1998-09-30					
; EARLIER APPLICATION NUMBER: 60/108,109					
; EARLIER FILING DATE: 1998-11-12					
; EARLIER APPLICATION NUMBER: 60/110,749					
; EARLIER FILING DATE: 1998-12-03					
; EARLIER APPLICATION NUMBER: 60/113,002					
; EARLIER FILING DATE: 1998-12-18					
; EARLIER APPLICATION NUMBER: 60/135,426					
; EARLIER FILING DATE: 1999-05-21					
; EARLIER APPLICATION NUMBER: 60/144,022					
; EARLIER FILING DATE: 1999-07-15					
; NUMBER OF SEQ ID NOS: 39					
; SOFTWARE: PatentIn Ver. 2.0					
; SEQ ID NO 4					
; LENGTH: 1536					
; TYPE: DNA					
; ORGANISM: Homo sapiens					
PCT-US99-22668-4					
Query Match 100.0%; Score 1535.6; DB 2; Length 1536;					
Best Local Similarity 100.0%; Pred. No. 0;					



QY 1081 CAGGATTTACAGTGCATTTCTGAAGAGAGAGACATCAACAGAAATAGGAGTTGTGCAACA 1140  
DB |||||  
QY 1081 CAGGATTTACAGTGCATTTCTGAAGAGAGAGACATCAACAGAAATAGGAGTTGTGCAACA 1140  
DB |||||  
QY 1141 GCTCTTTTGAGAGGAGGCGCTAAAGGACAGAGAGAAAGGTCCTCAATCGTGGAAAGAAAT 1200  
DB |||||  
QY 1201 TAAATGTTGATTAATAATAGATCAGAGTAGTTTCAGAGTTACCATGTAGTATTCACCT 1260  
DB |||||  
QY 1201 TAAATGTTGATTAATAATAGATCAGAGTAGTTTCAGAGTTACCATGTAGTATTCACCT 1260  
DB |||||  
QY 1261 AGCTGGGTTCTGATTTTCAGTTCCTTTCATACGGCTTAGGTAATGTCAAGGAGAAA 1320  
DB |||||  
QY 1261 AGCTGGGTTCTGATTTTCAGTTCCTTTCATACGGCTTAGGTAATGTCAAGGAGAAA 1320  
DB |||||  
QY 1321 AAACGTGCAAGTGAAGACCTGATTCGGTTGCGCTTAACTTAAAGCTCCATGTCCT 1380  
DB |||||  
QY 1321 AAACGTGCAAGTGAAGACCTGATTCGGTTGCGCTTAACTTAAAGCTCCATGTCCT 1380  
DB |||||  
QY 1381 GGGCTAAATTCGATTAATAATCTGATTTTTCATACGGCTTAGGTAATGTCAAGGAGAAA 1440  
DB |||||  
QY 1381 GGGCTAAATTCGATTAATAATCTGATTTTTCATACGGCTTAGGTAATGTCAAGGAGAAA 1440  
DB |||||  
QY 1441 TAAACCGAACAATTCATGTACTACTACAAACCTGGTTTAAAGGAACTATGTGCTATG 1500  
DB |||||  
QY 1441 TAAACCGAACAATTCATGTACTACTACAAACCTGGTTTAAAGGAACTATGTGCTATG 1500  
DB |||||  
QY 1501 AATTAACCTGTGTCATGCTGATAGGACAGACTGGA 1536  
DB |||||  
QY 1501 AATTAACCTGTGTCATGCTGATAGGACAGACTGGA 1536  
DB |||||

## RESULT 4

US-09-852-209-4

; Sequence 4, Application US/09852209

; GENERAL INFORMATION:

; APPLICANT: ERIKSSON, Ulf

; APPLICANT: AASE, Karin

; APPLICANT: LEE, Xuri

; APPLICANT: PONTEN, Annica

; APPLICANT: UUTELA, Marko

; APPLICANT: ALITALO, Kari

; APPLICANT: OESTMAN, Arne

; APPLICANT: HELDIN, Carl-Henrik

; APPLICANT: BEYSHOLTZ, Christer

; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING

; FILE OF INVENTION: THEREFOR, AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/852,209

; CURRENT FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: 09/410,349

; PRIOR FILING DATE: 1999-09-30

; PRIOR APPLICATION NUMBER: 60/110,749

; PRIOR FILING DATE: 1998-12-03

; PRIOR APPLICATION NUMBER: 60/113,002

; PRIOR FILING DATE: 1998-12-18

; PRIOR APPLICATION NUMBER: 60/135,426

; PRIOR FILING DATE: 1999-05-21

; PRIOR APPLICATION NUMBER: 60/144,022

; PRIOR FILING DATE: 1999-07-15

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 1536

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-852-209-4

Query Match

Best Local Similarity 100.0%; Score 1535.6; DB 35; Length 1536;

Matches 1536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGTAAATTTCCAGTCTTTCCAGCAACAGAGAAACGAGTACAAAGATCCTCAGCATG 60  
DB |||||  
QY 1 CGGGTAAATTTCCAGTCTTTCCAGCAACAGAGAAACGAGTACAAAGATCCTCAGCATG 60  
DB |||||  
QY 61 AGAGAATTAATTTACTGTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCATACTT 120  
DB |||||  
QY 61 AGAGAATTAATTTACTGTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCATACTT 120  
DB |||||  
QY 121 ATCCAGAAATACGGTCTTGGTATGGAGTTAGTACGAGTACAGGAAATGATGATAC 180  
DB |||||  
QY 121 ATCCAGAAATACGGTCTTGGTATGGAGTTAGTACGAGTACAGGAAATGATGATAC 180  
DB |||||  
QY 181 AACTTACGTTTGCATGAAGATTTGGCTTGAAGACCCAGAGATGACATATGCAAGTATG 240  
DB |||||  
QY 181 AACTTACGTTTGCATGAAGATTTGGCTTGAAGACCCAGAGATGACATATGCAAGTATG 240  
DB |||||  
QY 241 ATTTGTAGAGTTGAGGAAACCCAGTGTAGGAACTATATAGGGCGCTGGTGTGTTCTG 300  
DB |||||  
QY 241 ATTTGTAGAGTTGAGGAAACCCAGTGTAGGAACTATATAGGGCGCTGGTGTGTTCTG 300  
DB |||||  
QY 301 GTACTGTACCGAGAAACAGATTTCTTAAAGGAAATCCAAATTAGGATAAGATTTGATCTG 360  
DB |||||  
QY 301 GTACTGTACCGAGAAACAGATTTCTTAAAGGAAATCCAAATTAGGATAAGATTTGATCTG 360  
DB |||||  
QY 361 ATGAATATTTTCTTCTGAAACGAGGTTCTGCATCCACTTACCAATTTGTCATGCCACAAT 420  
DB |||||  
QY 361 ATGAATATTTTCTTCTGAAACGAGGTTCTGCATCCACTTACCAATTTGTCATGCCACAAT 420  
DB |||||  
QY 421 TCACAGAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGACCTTGGACCTGCTTA 480  
DB |||||  
QY 421 TCACAGAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGACCTTGGACCTGCTTA 480  
DB |||||  
QY 481 ATAATGCTATACTGCTTTTAGTACCTTGGAAAGACCTTATTCGATATCTTGAACACAGAGA 540  
DB |||||  
QY 481 ATAATGCTATACTGCTTTTAGTACCTTGGAAAGACCTTATTCGATATCTTGAACACAGAGA 540  
DB |||||  
QY 541 GATGGAGTTGAGCTTAGAAGATCTATATAGGCAACTTTGGCAACTTTCTTGGCAAGGCTT 600  
DB |||||  
QY 541 GATGGAGTTGAGCTTAGAAGATCTATATAGGCAACTTTGGCAACTTTCTTGGCAAGGCTT 600  
DB |||||  
QY 601 TTGTTTTTGGAGAAATCCAGAGTGTGAGTCTGAACTTCTTAAAGAGGAGGTAAGAT 660  
DB |||||  
QY 601 TTGTTTTTGGAGAAATCCAGAGTGTGAGTCTGAACTTCTTAAAGAGGAGGTAAGAT 660  
DB |||||  
QY 661 TATACAGCTGCACACCTGCTTAACTTCTCAGTGTCCATAAGGAAAGAACTTAAAGAGAACCG 720  
DB |||||  
QY 661 TATACAGCTGCACACCTGCTTAACTTCTCAGTGTCCATAAGGAAAGAACTTAAAGAGAACCG 720  
DB |||||  
QY 721 ATACCAATTTTCTGGCCAGGTTGCTCTGTTTAAAGCTGTGGTGGAACTGTGCTGTT 780  
DB |||||  
QY 721 ATACCAATTTTCTGGCCAGGTTGCTCTGTTTAAAGCTGTGGTGGAACTGTGCTGTT 780  
DB |||||  
QY 781 GTCTCCCAATTTGCAATGATGTCATGTCCTTGGAAAGAACTTAAAGAGAACCG 840  
DB |||||  
QY 781 GTCTCCCAATTTGCAATGATGTCATGTCCTTGGAAAGAACTTAAAGAGAACCG 840  
DB |||||  
QY 841 AGGTCTTTCAGTTGAGACCAAAACCGGTTGTCAGGGGATTCACAAATCACTCACCGAGC 900  
DB |||||  
QY 841 AGGTCTTTCAGTTGAGACCAAAACCGGTTGTCAGGGGATTCACAAATCACTCACCGAGC 900  
DB |||||  
QY 901 TGGCCCTGGAGCACCATGAGGAGTGTGCTGTGTCAGAGGAGGACACAGGAGATAGC 960  
DB |||||  
QY 901 TGGCCCTGGAGCACCATGAGGAGTGTGCTGTGTCAGAGGAGGACACAGGAGATAGC 960  
DB |||||  
QY 961 CGCATCAACCCAGCAGCTTTTCCAGAGCTGTGTCAGTGCAGTGCCTGATTTCTATTAGA 1020  
DB |||||  
QY 961 CGCATCAACCCAGCAGCTTTTCCAGAGCTGTGTCAGTGCAGTGCCTGATTTCTATTAGA 1020  
DB |||||  
QY 1021 GAACGATGCGTTATCTCCATCTCTTAACTCAGTTGTTGTTGCTTCAAGGACCTTCTATCTT 1080  
DB |||||  
QY 1021 GAACGATGCGTTATCTCCATCTCTTAACTCAGTTGTTGTTGCTTCAAGGACCTTCTATCTT 1080  
DB |||||  
QY 1081 CAGGATTTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACA 1140  
DB |||||

Db 1081 CAGGATTACAGTGCATTCTGAAAGAGGAGACATCAAAAGAGATTTAGGAGTTGTGCAACA 1140  
QY 1141 GCTCTTTTGAGAGAGCGCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAGAAAAT 1200  
Db 1141 GCTCTTTTGAGAGAGCGCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAGAAAAT 1200  
QY 1201 TAAATGTTGTTATTAATAGATCACAGCTAGTCTTTCAGAGTTTACCATGTACGTATTTCCACT 1260  
Db 1201 TAAATGTTGTTATTAATAGATCACAGCTAGTCTTTCAGAGTTTACCATGTACGTATTTCCACT 1260  
QY 1261 AGCTGGGTTCTGTTATTTCAAGTCTTTTCGATACGGCTTAGGGTAATGTCACTACAGGAAAA 1320  
Db 1261 AGCTGGGTTCTGTTATTTCAAGTCTTTTCGATACGGCTTAGGGTAATGTCACTACAGGAAAA 1320  
QY 1321 AAACGTGCAAGTGAGCACCTGATTCGTTGCGCTTGTCTTAACCTTAAGCTCCCATGTCCT 1380  
Db 1321 AAACGTGCAAGTGAGCACCTGATTCGTTGCGCTTGTCTTAACCTTAAGCTCCCATGTCCT 1380  
QY 1381 GGGCTAAAATCGTATTAATCTGGAATTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATG 1440  
Db 1381 GGGCTAAAATCGTATTAATCTGGAATTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATG 1440  
QY 1441 TAAACAGACATCTATGTAACATAACCTGCTTTTAAAAAGGAACATATGTTGCTATG 1500  
Db 1441 TAAACAGACATCTATGTAACATAACCTGCTTTTAAAAAGGAACATATGTTGCTATG 1500  
QY 1501 AATTAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536  
Db 1501 AATTAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536

## RESULT 5

us-09-852-209a-4  
; Sequence 4, Application US/09852209A  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: VUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETHSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/852,209A  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1536  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-852-209a-4

Query Match 100.0%; Score 1535.6; DB 35; Length 1536;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGTAAATCCAGTTTCCAGCAACAGGAACAGAACGAGTACAAAGATCTTCAGCATG 60

Db 1 CGGGTAAATCCAGTTTCCAGCAACAGGAACAGAACGAGTACAAAGATCTTCAGCATG 60  
QY 61 AGAGAAATTAATACGTGCTCTAATAATGAAAGTATTCACAGCCCAAGGTTTCTCATACTT 120  
Db 61 AGAGAAATTAATACGTGCTCTAATAATGAAAGTATTCACAGCCCAAGGTTTCTCATACTT 120  
QY 121 ATCCAGAAATACGGTCTTGGTATGGAGATTTAGTACAGTACAGGAAAAATGTATGGATAC 180  
Db 121 ATCCAGAAATACGGTCTTGGTATGGAGATTTAGTACAGTACAGGAAAAATGTATGGATAC 180  
QY 181 AACTTACGTTTGTATGAAAGATTTGGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATG 240  
Db 181 AACTTACGTTTGTATGAAAGATTTGGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATG 240  
QY 241 ATTTTGTAGAAATGAGGAAACCCAGTGAATATATATAGGGCGTGTGGTGTCTG 300  
Db 241 ATTTTGTAGAAATGAGGAAACCCAGTGAATATATATAGGGCGTGTGGTGTCTG 300  
QY 301 GTACTGTACCAAGGAAACAGATTTCTAAAGGAATCAAAATAGGATAGATTTCTATCTG 360  
Db 301 GTACTGTACCAAGGAAACAGATTTCTAAAGGAATCAAAATAGGATAGATTTCTATCTG 360  
QY 361 ATGAATATTTTCTTCTGAACCCAGGGTTCTGCATCCACTACAAATTTGTATGCCAAT 420  
Db 361 ATGAATATTTTCTTCTGAACCCAGGGTTCTGCATCCACTACAAATTTGTATGCCAAT 420  
QY 421 TCACAGAACTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCGCACTGCACTGCTTA 480  
Db 421 TCACAGAACTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCGCACTGCACTGCTTA 480  
QY 481 ATAATGCTATAACTTGCCTTTAGTACCTTTGGAAGACCTTTATCGATATCTTGAACAGAGA 540  
Db 481 ATAATGCTATAACTTGCCTTTAGTACCTTTGGAAGACCTTTATCGATATCTTGAACAGAGA 540  
QY 541 GATGGCAGTTGGACTTTAGAAATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTT 600  
Db 541 GATGGCAGTTGGACTTTAGAAATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTT 600  
QY 601 TTGTTTTTGAAGAAAATCCAGAGTGGTGTATCTGAACCTTCTTAAACAGAGAGGTAAGAT 660  
Db 601 TTGTTTTTGAAGAAAATCCAGAGTGGTGTATCTGAACCTTCTTAAACAGAGAGGTAAGAT 660  
QY 661 TATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAGAACTTAAGAGAACCG 720  
Db 661 TATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAGAACTTAAGAGAACCG 720  
QY 721 ATACCAATTTTCTGGCCAGGTTGTCTCCTGTTTAAACGCTGTGGTGGAACTGTGCCCTGTT 780  
Db 721 ATACCAATTTTCTGGCCAGGTTGTCTCCTGTTTAAACGCTGTGGTGGAACTGTGCCCTGTT 780  
QY 781 GTCTCCACAAATTCGAATGAATGTCAATGTGTCCAGCAAGGTTTCTAAATAATACACG 840  
Db 781 GTCTCCACAAATTCGAATGAATGTCAATGTGTCCAGCAAGGTTTCTAAATAATACACG 840  
QY 841 AGGTCTCTTCAGTTGAGACCAAAACCGGTGTGAGGGATTTGCAAAATCACTCACCACG 900  
Db 841 AGGTCTCTTCAGTTGAGACCAAAACCGGTGTGAGGGATTTGCAAAATCACTCACCACG 900  
QY 901 TGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGATAGC 960  
Db 901 TGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGATAGC 960  
QY 961 CGCATCACCAACAGAGCTCTTGGCCAGAGCTGTGAGTGTGTCAGTGTGCTGATTTCTATAGA 1020  
Db 961 CGCATCACCAACAGAGCTCTTGGCCAGAGCTGTGAGTGTGTCAGTGTGCTGATTTCTATAGA 1020  
QY 1021 GAAAGTATCGTTTATCTCCATCTTCAATCTCAGTTGTTTGTCTTCAAGGACCTTTCTATCT 1080  
Db 1021 GAAAGTATCGTTTATCTCCATCTTCAATCTCAGTTGTTTGTCTTCAAGGACCTTTCTATCT 1080  
QY 1081 CAGGATTTTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACA 1140





[illegible]

## RESULT 7

```

US-10-303-997B-4
; Sequence 4, Application US/10303997B
; GENERAL INFORMATION:
; APPLICANT: LI, Xuzi
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMELIET, Peter
; APPLICANT: COLLUM, Desire
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN
; FILE REFERENCE: 029085.44740C3
; CURRENT APPLICATION NUMBER: US/10/303,997B
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 60/102,461
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-997B-4

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	Query Match	100.0%;	Score 1535.6;	DB 50;	Length 1536;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1536;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	1	CGGGTAAATTC	CAGTTTTT	CCAGCAACAGGAACAGAGTACCAAGATCCTCAGCATG	60
Db	1	CGGGTAAATTC	CAGTTTTT	CCAGCAACAGGAACAGAGTACCAAGATCCTCAGCATG	60

QY	61	AGAGAATTATTACTGTGCTCTACTAATGGAAGATTTCACAGCCCAAGGTTTCCTCATACTT	120
DB	61	AGAGAATTATTACTGTGCTCTACTAATGGAAGATTTCACAGCCCAAGGTTTCCTCATACTT	120
QY	121	ATCCCAAGAAATACGGTCTTGGTATCGAGATTAGTAGCAGTACAGGAAATGTATCGATAC	180
DB	121	ATCCCAAGAAATACGGTCTTGGTATCGAGATTAGTAGCAGTACAGGAAATGTATCGATAC	180
QY	181	AACTTACGTTTGATGAAAGATTTTGGCTTTGAAGCCCAAGAAATGACATATGCAAGTATG	240
DB	181	AACTTACGTTTGATGAAAGATTTTGGCTTTGAAGCCCAAGAAATGACATATGCAAGTATG	240
QY	241	ATTTTGTAGAAGTTGAGGAAACCCAGTGTATGGAATATATATAGGGCGCTGGTGTGCTTG	300
DB	241	ATTTTGTAGAAGTTGAGGAAACCCAGTGTATGGAATATATATAGGGCGCTGGTGTGCTTG	300
QY	301	GTACTGTACCAAGGAAACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTGTGTATCTG	360
DB	301	GTACTGTACCAAGGAAACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTGTGTATCTG	360
QY	361	ATGAATATTTTCCCTCTGAAACGAGGTTCTGCATCCACTACAAATTTGTATGCCACAAT	420
DB	361	ATGAATATTTTCCCTCTGAAACGAGGTTCTGCATCCACTACAAATTTGTATGCCACAAT	420
QY	421	TCACAGAACTGTGAGTCCCTTCAGTGTCTACCCCTTCAGCTTTGCACTGCACCTGCTTA	480
DB	421	TCACAGAACTGTGAGTCCCTTCAGTGTCTACCCCTTCAGCTTTGCACTGCACCTGCTTA	480
QY	481	ATAATGCTATTAACCTGCTTTAGTACTTTGGAAGACCTTAATTCGATATCTTGAACACAG	540
DB	481	ATAATGCTATTAACCTGCTTTAGTACTTTGGAAGACCTTAATTCGATATCTTGAACACAG	540
QY	541	GATGGCAGTTGCACTTGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTT	600
DB	541	GATGGCAGTTGCACTTGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTT	600
QY	601	TTGTTTTTGGAAAGAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGGAGGTAAAGT	660
DB	601	TTGTTTTTGGAAAGAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGGAGGTAAAGT	660
QY	661	TATACAGTCGACACCTCGTAACCTTCAGTGTCCATAAGGGAAGAACTAAAGAAACCG	720
DB	661	TATACAGTCGACACCTCGTAACCTTCAGTGTCCATAAGGGAAGAACTAAAGAAACCG	720
QY	721	ATACCATTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGTGTGGGAACTGTGCCCTGT	780
DB	721	ATACCATTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGTGTGGGAACTGTGCCCTGT	780
QY	781	GTCTCCCAATTTGCAATGAATGTCAATGTGTCTCCCAAGCAAAAGTTACTATAAAATACC	840
DB	781	GTCTCCCAATTTGCAATGAATGTCAATGTGTCTCCCAAGCAAAAGTTACTATAAAATACC	840
QY	841	AGGTCCCTTCAGTTGAGACCAAAACCGGTGTACGGGANTGCAAAATCACTCACCGACG	900
DB	841	AGGTCCCTTCAGTTGAGACCAAAACCGGTGTACGGGANTGCAAAATCACTCACCGACG	900
QY	901	TGGCCCTGAGACCAATGAGGAGTGTGACTGTGTGTGACAGGGAGGACACAGGAGTACG	960
DB	901	TGGCCCTGAGACCAATGAGGAGTGTGACTGTGTGTGACAGGGAGGACACAGGAGTACG	960
QY	961	CGCATCACCAACAGCAGCTCTTCCCGACAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTG	1020
DB	961	CGCATCACCAACAGCAGCTCTTCCCGACAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTG	1020
QY	1021	GACAGTATGCGTTATCTCCATCCTTAATCTCAGTTGTGTTTTCCTCAAGGACCTTTCATCT	1080
DB	1021	GACAGTATGCGTTATCTCCATCCTTAATCTCAGTTGTGTTTTCCTCAAGGACCTTTCATCT	1080
QY	1081	CAGGATTTACAGTGCATTTCTGAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACA	1140
DB	1081	CAGGATTTACAGTGCATTTCTGAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACA	1140



1141 GCTCTTTTGAGAGAGGCGCTTAAAGGACAGAGGAAAGGCTCTCAATCGTGGAAAGAAAT 1200  
1141 GCTCTTTTGAGAGAGGCGCTTAAAGGACAGAGGAAAGGCTCTCAATCGTGGAAAGAAAT 1200  
1201 TAAATGTTGTTAATAATAGATACACAGCTAGTTTTCAGAGTTACCATGTAGTATCCACT 1260  
1201 TAAATGTTGTTAATAATAGATACACAGCTAGTTTTCAGAGTTACCATGTAGTATCCACT 1260  
1261 AGCTGGGTTCTGTTATTTCACTTCTTTCGATACGCGCTTAGGGTAAATGTCAAGGAAA 1320  
1261 AGCTGGGTTCTGTTATTTCACTTCTTTCGATACGCGCTTAGGGTAAATGTCAAGGAAA 1320  
1321 AACTGTGCAAGTGAGCACCTGATTCGCTTGCCCTTAACTTAAAGCTCCATGTCTCT 1380  
1321 AACTGTGCAAGTGAGCACCTGATTCGCTTGCCCTTAACTTAAAGCTCCATGTCTCT 1380  
1381 GGGCTTAAATCGTATATAATCTGATTTTTTTTTTTTTTTTTTTTTTTCCTCATATG 1440  
1381 GGGCTTAAATCGTATATAATCTGATTTTTTTTTTTTTTTTTTTTTTTCCTCATATG 1440  
1441 TAAACCGAAGCATCTATGATCTACCAACCTGGTTTTTAAAGGAACTATGTTGCTATG 1500  
1441 TAAACCGAAGCATCTATGATCTACCAACCTGGTTTTTAAAGGAACTATGTTGCTATG 1500  
1501 AATTAAACTTGTGTCATCTGCTGATAGGACAGACTGGA 1536  
1501 AATTAAACTTGTGTCATCTGCTGATAGGACAGACTGGA 1536

RESULT 8  
US-09-184-216-1  
; Sequence 1, Application US/09184216  
; GENERAL INFORMATION:  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Kuo, Sophia S.  
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1  
; FILE REFERENCE: P1122P1  
; CURRENT APPLICATION NUMBER: US/09/184,216  
; CURRENT FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 1  
; LENGTH: 2825  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: Unknown  
; LOCATION: 2689  
; OTHER INFORMATION: Any nucleotide  
US-09-184-216-1

Query Match 99.8%; Score 1532.6; DB 16; Length 2825;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GTAAATCCAGTTTCCAGCAACAGGAAACAGAGCGAGTCAAGATCCTCAGCATGAGA 63  
DB 341 GTAAATCCAGTTTCCAGCAACAGGAAACAGAGCGAGTCAAGATCCTCAGCATGAGA 400  
QY 64 GAATTTACTGTGTCTACTAATGGAAGTATTCACGCCAAGGTTTCTCATCTATC 123  
DB 401 GAATTTACTGTGTCTACTAATGGAAGTATTCACGCCAAGGTTTCTCATCTATC 460  
QY 124 CAAGAAATACCGTCTTGTGTATGGAGTTAGTACGATGAGGAAATCTATGGATCAAC 183  
DB 461 CAAGAAATACCGTCTTGTGTATGGAGTTAGTACGATGAGGAAATCTATGGATCAAC 520  
QY 184 TTACGTTTGTGATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGATGATT 243  
DB 521 TTACGTTTGTGATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGATGATT 580  
QY 244 TTGTAGAGTTGAGGAAACCCAGTGTGAACTATATTAAGGCGCTGTGTGCTGTGTA 303  
DB 581 TTGTAGAGTTGAGGAAACCCAGTGTGAACTATATTAAGGCGCTGTGTGCTGTGTA 640

QY 304 CTGTACCAAGGAAAACAGATTTTCTTAAAGGAAATCAAATTTAGGATAGATTTGTATCTGATG 363  
DB 641 CTGTACCAAGGAAAACAGATTTTCTTAAAGGAAATCAAATTTAGGATAGATTTGTATCTGATG 700  
QY 364 AATATTTTCTTCTGAAACAGGTTTCTGCATCCACTCAACAATTTGCACAAATTTCA 423  
DB 701 AATATTTTCTTCTGAAACAGGTTTCTGCATCCACTCAACAATTTGCACAAATTTCA 760  
QY 424 CAGAAAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCCACTGACCTGCTTAATA 483  
DB 761 CAGAAAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCCACTGACCTGCTTAATA 820  
QY 484 ATGCTTATAACTGCCCTTTAGTACTTTGGAAGACCTTTATTCGATATCTTGAACACAGAGAGAT 543  
DB 821 ATGCTTATAACTGCCCTTTAGTACTTTGGAAGACCTTTATTCGATATCTTGAACACAGAGAGAT 880  
QY 544 GGCAGTTGAGCTTTGAGAAATCTATATAGCCAACTTTGCAACTCTTCTGCAAGGCTTTTG 603  
DB 881 GGCAGTTGAGCTTTGAGAAATCTATATAGCCAACTTTGCAACTCTTCTGCAAGGCTTTTG 940  
QY 604 TTTTGGAGAGAAATCCAGAGTGGTGGATCTCAACCTTCTAACAGAGAGGTAAGATTAT 663  
DB 941 TTTTGGAGAGAAATCCAGAGTGGTGGATCTCAACCTTCTAACAGAGAGGTAAGATTAT 1000  
QY 664 ACAGCTGCAACCTCTGTAACTTCTCAGTGTCCATAGGAGAACTAAAGAAACCGATA 723  
DB 1001 ACAGCTGCAACCTCTGTAACTTCTCAGTGTCCATAGGAGAACTAAAGAAACCGATA 1060  
QY 724 CCATTTTCTGGCCAGGTTGTCTCTCTGTTAAACGCTGTGTGGGAACTGTGCTCTGTC 783  
DB 1061 CCATTTTCTGGCCAGGTTGTCTCTCTGTTAAACGCTGTGTGGGAACTGTGCTCTGTC 1120  
QY 784 TCCACAAATTCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 843  
DB 1121 TCCACAAATTCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1180  
QY 844 TCCTTCAGTTGAGACCAAAASACCGTGTTCAGGGGATTTGCACAAATCACTCAGGAGTGG 903  
DB 1181 TCCTTCAGTTGAGACCAAAASACCGTGTTCAGGGGATTTGCACAAATCACTCAGGAGTGG 1240  
QY 904 CCCTGGAGCACCATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 963  
DB 1241 CCCTGGAGCACCATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1300  
QY 964 ATCACCACAGCAGCTCTTTCGCCAGAGCTGTGCGAGTGTGCGTGTGCTGATTTCTATTAGAGAA 1023  
DB 1301 ATCACCACAGCAGCTCTTTCGCCAGAGCTGTGCGAGTGTGCGTGTGCTGATTTCTATTAGAGAA 1360  
QY 1024 CGTATCGGTTATCTCCATCTTAATCTCAGTTGTTTGTCTTCAAGGACCTTTCTATCTTCAG 1083  
DB 1361 CGTATCGGTTATCTCCATCTTAATCTCAGTTGTTTGTCTTCAAGGACCTTTCTATCTTCAG 1420  
QY 1084 GATTTACAGTGTGATCTTGAAGAGGAGACATCAAAACAGAAATTTAGGAGTTGTGCAACAGCT 1143  
DB 1421 GATTTACAGTGTGATCTTGAAGAGGAGACATCAAAACAGAAATTTAGGAGTTGTGCAACAGCT 1480  
QY 1144 CTTTTCAGAGGAGGCTTAAAGGAGAGGAGAAAGGCTTCTCAATCGTGGGAAAGAAATTTAA 1203  
DB 1481 CTTTTCAGAGGAGGCTTAAAGGAGAGGAGAAAGGCTTCTCAATCGTGGGAAAGAAATTTAA 1540  
QY 1204 ATGCTGTATTAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTTATTTCCATGAG 1263  
DB 1541 ATGCTGTATTAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTTATTTCCATGAG 1600  
QY 1264 TGGGTTCTGTATTTTCAAGTTCTTTTCGATACGGCTTTAGGGTAAATGTGATGATCAGGAAAAAA 1323  
DB 1601 TGGGTTCTGTATTTTCAAGTTCTTTTCGATACGGCTTTAGGGTAAATGTGATGATCAGGAAAAAA 1660  
QY 1324 CTGTGCAAGTGTGAGCACCTGATTCGCTTGTGCTTAACTCTAAAGCTCCATGCTCTGCTGG 1383  
DB 1661 CTGTGCAAGTGTGAGCACCTGATTCGCTTGTGCTTAACTCTAAAGCTCCATGCTCTGCTGG 1720

QY 1384 CCTAAATCGTATATAAATCTGGATTTTTTTTTTTTTTTTTTTTTTTTGGTCTCATATTCACATATGTAA 1443  
Db 1721 CCTAAATCGTATATAAATCTGGATTTTTTTTTTTTTTTTTTTTTTTGCTCATATTCACATATGTAA 1780  
QY 1444 ACCAGACATCTATGATCTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATGAAT 1503  
Db 1781 ACCAGACATCTATGATCTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATGAAT 1840  
QY 1504 TAAACTTGTGTCTATGCTATAGGACAGACTGGA 1536  
Db 1841 TAAACTTGTGTCTATGCTATAGGACAGACTGGA 1873

RESULT 9  
US-09-723-749-1  
; Sequence 1, Application US/09723749  
; GENERAL INFORMATION:  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Kuo, Sophia S.  
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1  
; FILE REFERENCE: P1122P2D1  
; CURRENT APPLICATION NUMBER: US/09/723,749  
; PRIORITY FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: US 09/265,686  
; PRIOR FILING DATE: 1999-03-10  
; PRIOR APPLICATION NUMBER: US 09/040,220  
; PRIOR FILING DATE: 1998-03-17  
; PRIOR APPLICATION NUMBER: US 09/184,216  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 1  
; LENGTH: 2825  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: Unknown  
; LOCATION: 2689  
; OTHER INFORMATION: Any nucleotide  
US-09-723-749-1

Query Match 99.8%; Score 1532.6; DB 32; Length 2825;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTAAATTCAGTTTTCCAGCAACAGGACGAGTCAAGATCCTCAGCATGAGA 63  
Db 341 GTAAATTCAGTTTTCCAGCAACAGGACGAGTCAAGATCCTCAGCATGAGA 400  
QY 64 GAATTTACTGTCTACTAATGAGTATTCACAGCCAGGTTTCTCATCTTATC 123  
Db 401 GAATTTACTGTCTACTAATGAGTATTCACAGCCAGGTTTCTCATCTTATC 460  
QY 124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 183  
Db 461 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 520  
QY 184 TTACCTTTGATCAAGATTTGGCTTTGAAGCCAGAGATGACATATGCAAGTATGATT 243  
Db 521 TTACCTTTGATCAAGATTTGGCTTTGAAGCCAGAGATGACATATGCAAGTATGATT 580  
QY 244 TTGTAGAAAGTTGAGGAAACCCAGTGTGAACCTATATTAGGGCGCTGGTGTCTGGTA 303  
Db 581 TTGTAGAAAGTTGAGGAAACCCAGTGTGAACCTATATTAGGGCGCTGGTGTCTGGTA 640  
QY 304 CTGTACAGGAAACAGATTTCTAAAGGAAATCAAAATAGGATAGATTTGTATCTGATG 363  
Db 641 CTGTACAGGAAACAGATTTCTAAAGGAAATCAAAATAGGATAGATTTGTATCTGATG 700  
QY 364 AATATTTTCTCTGAAACAGGTTTCTGCATCCACTACAACATTTCTCATGCCAATTC 423  
Db 701 AATATTTTCTCTGAAACAGGTTTCTGCATCCACTACAACATTTCTCATGCCAATTC 460  
QY 424 CAGAAGCTGTAGTCTTCCAGTGTGCTACCCCTTCCAGTCTTCCACTGACCTGCTTAATA 483

Db 761 CAGAAGCTGTAGTCTTCCAGTGTGCTACCCCTTCCAGTCTGCACTGCACTGCTTAATA 820  
QY 484 ATGCTATAACTGCTTTAGTACCTTTGGAAGACCTTTATTCGATATCTTGAACAGAGAGAT 543  
Db 821 ATGCTATAACTGCTTTAGTACCTTTGGAAGACCTTTATTCGATATCTTGAACAGAGAGAT 880  
QY 544 GGCAGTTGACATTAAGATCTATATAGGCACTTGGCACTTCTGCAAGGCTTGGCAGGCTTTG 603  
Db 881 GGCAGTTGACATTAAGATCTATATAGGCACTTGGCACTTCTGCAAGGCTTGGCAGGCTTTG 940  
QY 604 TTTTGGAAAGAAATCCAGAGTGGTGGATCTCAACCTTCTAACAGAGAGGTAAGATTAAT 663  
Db 941 TTTTGGAAAGAAATCCAGAGTGGTGGATCTCAACCTTCTAACAGAGAGGTAAGATTAAT 1000  
QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCTATAGGGAAGAACTAAAGAAACCGATA 723  
Db 1001 ACAGCTGCACACCTCGTAACTTCTCAGTGTCTATAGGGAAGAACTAAAGAAACCGATA 1060  
QY 724 CCATTTTCTGGCCAGGTTCTCTCTGTTTAAACGCTTGGTGGAACTGTGCTGTGTTC 783  
Db 1061 CCATTTTCTGGCCAGGTTCTCTCTGTTTAAACGCTTGGTGGAACTGTGCTGTGTTC 1120  
QY 784 TCCACAATTTGCAATGAATGTCAATGTCTCCCAAGCAAAAGTTTACTAAAAATACCAAGG 843  
Db 1121 TCCACAATTTGCAATGAATGTCAATGTCTCCCAAGCAAAAGTTTACTAAAAATACCAAGG 1180  
QY 844 TCCCTCAGTTGAGACCAAAACGCTGTCAGGGGATTCACAAATCACTCACCGAGCTGG 903  
Db 1181 TCCCTCAGTTGAGACCAAAACGCTGTCAGGGGATTCACAAATCACTCACCGAGCTGG 1240  
QY 904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCAAGAGAGATAGCCGC 963  
Db 1241 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCAAGAGAGATAGCCGC 1300  
QY 964 ATCAACACAGAGCTCTTCCAGAGCTGTCGAGTGCAGTGGCTGATTTCTATTAGAGAA 1023  
Db 1301 ATCAACACAGAGCTCTTCCAGAGCTGTCGAGTGCAGTGGCTGATTTCTATTAGAGAA 1360  
QY 1024 CGTATGCTTATCTCCATCTTAATCTCAGTTGTGTTTGTCTTCAAGGACCTTTTCACTTTCAG 1083  
Db 1361 CGTATGCTTATCTCCATCTTAATCTCAGTTGTGTTTGTCTTCAAGGACCTTTTCACTTTCAG 1420  
QY 1084 GATTTACAGTGCATCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACGCT 1143  
Db 1421 GATTTACAGTGCATCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACGCT 1480  
QY 1144 CTTTTCAGAGGAGGCTTAAAGGACAGGAAAGGCTTCAATCGTGGAAAGAAATTA 1203  
Db 1481 CTTTTCAGAGGAGGCTTAAAGGACAGGAAAGGCTTCAATCGTGGAAAGAAATTA 1540  
QY 1204 ATGTTGTATTAAATAGATCACCAGCTAGTTTTCAGAGTTTACCATGTACGTTATTCACATG 1263  
Db 1541 ATGTTGTATTAAATAGATCACCAGCTAGTTTTCAGAGTTTACCATGTACGTTATTCACATG 1600  
QY 1264 TGGGTTCTGTATTTCAGTTCTTTCGATACGCTTGGTAACTTCAAGTACAGGAAATAA 1323  
Db 1601 TGGGTTCTGTATTTCAGTTCTTTCGATACGCTTGGTAACTTCAAGTACAGGAAATAA 1660  
QY 1324 CTGTCAAGTGTAGCACCTGATTCGCTTGGCTTTAACTCTTAAAGCTCCATGTCTCTGGG 1383  
Db 1661 CTGTCAAGTGTAGCACCTGATTCGCTTGGCTTTAACTCTTAAAGCTCCATGTCTCTGGG 1720  
QY 1384 CTTAAATCTGTATAAATCTGGATTTTTTTTTTTTTTTTTTGTCTCATATTTCATATGTAA 1443  
Db 1721 CTTAAATCTGTATAAATCTGGATTTTTTTTTTTTTTTTTTGTCTCATATTTCATATGTAA 1780  
QY 1444 ACCAGAACATTTCTATGCTACAAACCTGTTTTTAAAGGAACTATGTTGCTATGAAT 1503  
Db 1781 ACCAGAACATTTCTATGCTACAAACCTGTTTTTAAAGGAACTATGTTGCTATGAAT 1840  
QY 1504 TAAACTTGTGTCTATGCTATAGGACAGACTGGA 1536

Db 1841 TAAACTTGTCTGCTGCTGATAGGACAGACTGGA 1873

RESULT 10  
US-10-178-442-1  
; Sequence 1, Application US/10178442  
; GENERAL INFORMATION:  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Ferrara, Napoleone  
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1  
; FILE REFERENCE: 11669.112USD2  
; CURRENT APPLICATION NUMBER: US/10178.442  
; CURRENT FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: US 09/265,686  
; PRIOR FILING DATE: 1999-03-10  
; PRIOR APPLICATION NUMBER: US 09/184,216  
; PRIOR FILING DATE: 1998-11-02  
; PRIOR APPLICATION NUMBER: US 09/040,220  
; PRIOR FILING DATE: 1998-03-17  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2825  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2689)..(2689)  
; OTHER INFORMATION: Any nucleotide  
US-10-178-442-1

Query Match 99.8%; Score 1532.6; DB 47; Length 2825;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTAAATTCAGTTTCCAGCAACAGGACAGAGGATACAGAGTCCCTCAGATCAGA 63  
Db 341 GTAAATTCAGTTTCCAGCAACAGGACAGAGGATACAGAGTCCCTCAGATCAGA 400

QY 64 GAATTTATTTACTGTCTACTAATGAAGTATTCACAGCCCAAGGTTTCTCATCTTATC 123  
Db 401 GAATTTATTTACTGTCTACTAATGAAGTATTCACAGCCCAAGGTTTCTCATCTTATC 460

QY 124 CAAGAAATACCGTCTTGTGTATGAGATTTAGTACAGTACAGGAAATGTATGATCAAC 183  
Db 461 CAAGAAATACCGTCTTGTGTATGAGATTTAGTACAGTACAGGAAATGTATGATCAAC 520

QY 184 TTACGTTTGTATGATGAAAGTTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGAT 243  
Db 521 TTACGTTTGTATGATGAAAGTTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGAT 580

QY 244 TTGTAGAGTTTGAAGACCCAGTGTATGAACTATATAGGCGCTGTGTCTGTTA 303  
Db 581 TTGTAGAGTTTGAAGACCCAGTGTATGAACTATATAGGCGCTGTGTCTGTTA 640

QY 304 CTGTACCAAGGAAACAGATTTCTAAGGAAATCAAAATAGGATAAGATTTGTATCTCATG 363  
Db 641 CTGTACCAAGGAAACAGATTTCTAAGGAAATCAAAATAGGATAAGATTTGTATCTCATG 700

QY 364 AATATTTCTTCTGAAACAGAGTTTCTGCATCCACTACAAATTTGTATGATGCAATCA 423  
Db 701 AATATTTCTTCTGAAACAGAGTTTCTGCATCCACTACAAATTTGTATGATGCAATCA 760

QY 424 CAGAAGCTGTAGTCTTCTGAGTCTACCCCTTCCAGCTTTCAGCTTTCGACCTGCTTAATA 483  
Db 761 CAGAAGCTGTAGTCTTCTGAGTCTACCCCTTCCAGCTTTCGACCTGCTTAATA 820

QY 484 ATGCTATAACCTGCTTTAGTACCTTGGAGACCTTATTCGATATCTTTGAACAGAGAT 543  
Db 821 ATGCTATAACCTGCTTTAGTACCTTGGAGACCTTATTCGATATCTTTGAACAGAGAT 880

QY 544 GGCAGTTCGACTTAGAAGATCTATATAGGCCCACTTGGCACTTCTTGGCAGGCTTTTG 603

Db 881 GGCAGTTCGACTTAGAAGATCTATATAGGCCCACTTGGCACTTCTTGGCAGGCTTTTG 940

QY 604 TTTTGGAGAGAAATCCAGAGTGGTGGATCTGAACTTCTAAACAGAGAGGTAAAGATTAT 663

Db 941 TTTTGGAGAGAAATCCAGAGTGGTGGATCTGAACTTCTAAACAGAGAGGTAAAGATTAT 1000

QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGAGAACTAAAGAGAACCGATA 723

Db 1001 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGAGAACTAAAGAGAACCGATA 1060

QY 724 CCATTTCTGGCCAGGTTCTCTCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGTGC 783

Db 1061 CCATTTCTGGCCAGGTTCTCTCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGTGC 1120

QY 784 TCCACAAATTCGAATGAACTGTGCTCCCAAGCAAAAGTTACTAAATAATACCCAGG 843

Db 1121 TCCACAAATTCGAATGAACTGTGCTCCCAAGCAAAAGTTACTAAATAATACCCAGG 1180

QY 844 TCCTTCAGTTGAGACCAAAACCCGCTGTCCAGGGGATTCACAAATCACTCACCGAGTGG 903

Db 1181 TCCTTCAGTTGAGACCAAAACCCGCTGTCCAGGGGATTCACAAATCACTCACCGAGTGG 1240

QY 904 CCCTGAGCACCATGAGGAGTGTGCTGTGTCAGAGGAGGACAGAGATACCGC 963

Db 1241 CCCTGAGCACCATGAGGAGTGTGCTGTGTCAGAGGAGGACAGAGATACCGC 1300

QY 964 ATCACCACAGCAGCTCTTCCAGAGCTGTGTCAGTGCAGTGGCTGATTCTATTAGAGAA 1023

Db 1301 ATCACCACAGCAGCTCTTCCAGAGCTGTGTCAGTGCAGTGGCTGATTCTATTAGAGAA 1360

QY 1024 CGTATCGGTTATCTCCATCTTAATCTCAGTTGTTTCTTCAAGGACCTTTTCTCTTCA 1083

Db 1361 CGTATCGGTTATCTCCATCTTAATCTCAGTTGTTTCTTCAAGGACCTTTTCTCTTCA 1420

QY 1084 GATTTACGTGATCTCTGAAAGAGGAGACATCAAAACAGAAATTTAGGAGTTGTCCACAGCT 1143

Db 1421 GATTTACGTGATCTCTGAAAGAGGAGACATCAAAACAGAAATTTAGGAGTTGTCCACAGCT 1480

QY 1144 CTTTTCAGAGGAGGCTTAAAGGACAGGAGAAAGGCTTCTCAATCGTGGAGAAATTTAA 1203

Db 1481 CTTTTCAGAGGAGGCTTAAAGGACAGGAGAAAGGCTTCTCAATCGTGGAGAAATTTAA 1540

QY 1204 ATGTTGTATTAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCTAGC 1263

Db 1541 ATGTTGTATTAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCTAGC 1600

QY 1264 TGGGTTCTGTATTTTCAAGTTCTTTTCGATACGGCTTAGGGTAATGTCACTACAGGAAAAA 1323

Db 1601 TGGGTTCTGTATTTTCAAGTTCTTTTCGATACGGCTTAGGGTAATGTCACTACAGGAAAAA 1660

QY 1324 CTGTGAGTGCAGCCTGATTCGGTTCCTTTCGATACCTTAAGCTCCATGTCTGGG 1383

Db 1661 CTGTGAGTGCAGCCTGATTCGGTTCCTTTCGATACCTTAAGCTCCATGTCTGGG 1720

QY 1384 CTTAAATTCGTATAAATCTGGAATTTTTTTTTTTTTTTTTTTCATATTCATATGTA 1443

Db 1721 CTTAAATTCGTATAAATCTGGAATTTTTTTTTTTTTTTTTTTCATATTCATATGTA 1780

QY 1444 ACCAGAACCTTCTATGATCTACAAACCTGTTTAAAAAGGAACTATGTTCTGATGAT 1503

Db 1781 ACCAGAACCTTCTATGATCTACAAACCTGTTTAAAAAGGAACTATGTTCTGATGAT 1840

QY 1504 TAAACTTGTGCTCATGCTGATGAGCAGACTGGA 1536

Db 1841 TAAACTTGTGCTCATGCTGATGAGCAGACTGGA 1873

## RESULT 11

PCT-US01-43523-285  
; Sequence 285, Application PC/TUS0143523  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen

```

APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C331
CURRENT APPLICATION NUMBER: PCT/US01/43523
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 285
LENGTH: 2849
TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: unsure
LOCATION: 2715
OTHER INFORMATION: unknown base
PCT-US01-43523-285

Query Match 99.8%; Score 1532.6; DB 1; Length 2849;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTAAATTCAGTTTCCAGCAACAGGACAGGAGTACAGATCTCAGCATGAGA 63
Db 367 GTAAATTCAGTTTCCAGCAACAGGACAGGAGTACAGATCTCAGCATGAGA 426
QY 64 GAATATTACTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATCTATC 123
Db 427 GAATATTACTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATCTATC 486
QY 124 CAAGAAATACGTCCTTGGTATGAGATTAGTAGCAGTAGAGAAATATGATGATACAA 183
Db 487 CAAGAAATACGTCCTTGGTATGAGATTAGTAGCAGTAGAGAAATATGATGATACAA 546
QY 184 TTACGTTTGCATGAAGATTGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
Db 547 TTACGTTTGCATGAAGATTGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 606
QY 244 TTGTAGAGTTGAGGAACCCAGTGATGGAACATATATTAGGCGCTGGTGTCTGGTA 303

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Db 1387 CGTATCGTTATCTCCATCTTAATCTCAGTTGTTTGGCTTCAAGGACCTTTTCATCTTCAG 1446
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QY 1144 CTTTTCAGAGGAGCCCTAAAGGACAGGAGAAAGGCTTCAATCTGFGGAAAGAAATTA 1203
Db 1507 CTTTTCAGAGGAGCCCTAAAGGACAGGAGAAAGGCTTCAATCTGFGGAAAGAAATTA 1566
QY 1204 ATGCTGTATTAAATAGATCACCAAGTAGTTTTCAGAGTTACCATGTACGTATTCCTAGC 1263
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## RESULT 13

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PCT-US01-43523-285
; Sequence 285, Application PC/TUS0143523
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C331
; CURRENT APPLICATION NUMBER: PCT/US01/43523
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059122

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; PRIOR FILING DATE: 1997-09-17
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; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 285
; LENGTH: 2849
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2715
; OTHER INFORMATION: unknown base
PCT-US01-43523-285

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Query Match 99.8%; Score 1532.6; DB 2; Length 2849;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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/ PRIOR FILING DATE: 1998-09-11
/ NUMBER OF SEQ ID NOS: 538
/ SEQ ID NO 487
/ LENGTH: 2849
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: 2715
/ OTHER INFORMATION: unknown base
US-09-380-138-487

Query Match 99.8%; Score 1532.6; DB 20; Length 2849;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 427 GAATTTACTGTGTCTACTAATGAAGTATTTCAGCCCAAGGTTTCTCATCTTATC 486
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Qy |||||  
1504 TAAACTTGTCTATGCTGATAGGACAGACTGGA 1536  
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RESULT 2	US-10-648-593-58
;	Sequence 58, Application US/10648593
;	GENERAL INFORMATION:
;	APPLICANT: Bristol-Myers Squibb Company
;	TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES
;	TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES
;	TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
;	FILE REFERENCE: D0273 NP
;	CURRENT APPLICATION NUMBER: US/10/648,593
;	CURRENT FILING DATE: 2003-08-26
;	PRIOR APPLICATION NUMBER: 60/406,385
;	PRIOR FILING DATE: 2002-08-27
;	NUMBER OF SEQ ID NOS: 557
;	SOFTWARE: PatentIn version 3.2
;	SEQ ID NO 58
;	LENGTH: 3007
;	TYPE: DNA
;	ORGANISM: Homo sapiens
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Query Match          99.7%; Score 1531; DB 6; Length 3007;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 1531: Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy 1384 CCTAAAATCGTAAATCTGATTTTCTGATTTTCTGATTTTCTGATTTTCTGATTTTCTGAT 1443
Db 1954 CCTAAAATCGTAAATCTGATTTTCTGATTTTCTGATTTTCTGATTTTCTGATTTTCTGAT 2013
Qy 1444 ACCAGAACATCTATGTACTACAACTGTTTAAAGGAGAACTATGTTCTGATGAT 1503
Db 2014 ACCAGAACATCTATGTACTACAACTGTTTAAAGGAGAACTATGTTCTGATGAT 2073
Qy 1504 TAAACTTGTCTCATGCTGATGAGCAGACTGGA 1536
Db 2074 TAAACTTGTCTCATGCTGATGAGCAGACTGGA 2106
```

## RESULT 4

```
US-60-485-450-137
; Sequence 137, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 3007
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-485-450-137
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```
Query Match 99.7%; Score 1531; DB 7; Length 3007;
Best local similarity 99.7%; Pred. No. 0;
Matches 1526; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 4 GTAAATTCAGTTTCCAGCAACAGGAAACGAGTACAGATCCTCAGCATGAGA 63
Db 574 GTAAATTCAGTTTCCAGCAACAGGAAACGAGTACAGATCCTCAGCATGAGA 633
Qy 64 GAATTTATTAATCTGTGCTTACTTAATGGAAGTATTCACAGCCCAAGGTTTCTCATATCTATC 123
Db 634 GAATTTATTAATCTGTGCTTACTTAATGGAAGTATTCACAGCCCAAGGTTTCTCATATCTATC 693
Qy 124 CAAGAAATACCGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATGTATGATCAAC 183
Db 694 CAAGAAATACCGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATGTATGATCAAC 753
Qy 184 TTACGTTTGTATGAAGATTTTGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
Db 754 TTACGTTTGTATGAAGATTTTGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 813
Qy 244 TTGTAGAAGTTGAGGAAACCCAGATGATGAACTATATTTAGGGCGCTGGTGTGGTAT 303
Db 814 TTGTAGAAGTTGAGGAAACCCAGATGATGAACTATATTTAGGGCGCTGGTGTGGTAT 873
Qy 304 CTGTACAGAGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTTGTATCTGATG 363
Db 874 CTGTACAGAGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTTGTATCTGATG 933
Qy 364 AATATTTTCTTCTGAAACCCAGGGTTCTGATCCACTACAACTTGTCTATGCCCAATTC 423
Db 934 AATATTTTCTTCTGAAACCCAGGGTTCTGATCCACTACAACTTGTCTATGCCCAATTC 993
Qy 424 CAGAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCGCACTGGAACCTGCTTAA 483
Db 994 CAGAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCGCACTGGAACCTGCTTAA 1053
Qy 484 ATGCTATTAATCTGCTTGTAGTACCTTGAAGACCTTATTCGATATCTTGAACAGAGAGAT 543
Db 1054 ATGCTATTAATCTGCTTGTAGTACCTTGAAGACCTTATTCGATATCTTGAACAGAGAGAT 1113
Qy 544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTG 603
Db 1114 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTG 1173
Qy 604 TTTTGGAGAGAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGAGATGATAT 663
Db 1174 TTTTGGAGAGAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGAGATGATAT 1233
Qy 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAGAACTAAAGAGAACCGATA 723
Db 1234 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAGAACTAAAGAGAACCGATA 1293
Qy 724 CCATTTTCTGCGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGTC 783
Db 1294 CCATTTTCTGCGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGTC 1353
Qy 784 TCCCAATTTGCAATGAATGTCAATGTCTCCCAAGAAAGTTACTTAAATAATACCAAGG 843
Db 1354 TCCCAATTTGCAATGAATGTCAATGTCTCCCAAGAAAGTTACTTAAATAATACCAAGG 1413
Qy 844 TCCTTCAGTTGAGACCAAAACCCGTTGTGAGGAGTTGCAAAATCTACCCGACCTGG 903
Db 1414 TCCTTCAGTTGAGACCAAAACCCGTTGTGAGGAGTTGCAAAATCTACCCGACCTGG 1473
Qy 904 CCCTGGAGCACCATGAGGAGTGTGACCTGTGTGTCAGAGGGAGCACAGGAGTAGCCGC 963
Db 1474 CCCTGGAGCACCATGAGGAGTGTGACCTGTGTGTCAGAGGGAGCACAGGAGTAGCCGC 1533
Qy 964 ATCACCACAGCAGCTCTTGGCCAGAGCTGTGTCAGTGCAGTGGCTGATTCTATTAGAGAA 1023
Db 1534 ATCACCACAGCAGCTCTTGGCCAGAGCTGTGTCAGTGCAGTGGCTGATTCTATTAGAGAA 1593
Qy 1024 CGTATCGTTATCTCAATCTTAAATCTGATTTGCTTCAAGGACCTTTCATCTTCAG 1083
Db 1594 CRTATCGTTATCTCAATCTTAAATCTGATTTGCTTCAAGGACCTTTCATCTTCAG 1653
Qy 1084 GATTTACAGTGCATTTCTGAAAGAGGAGACATCAACAGAGATTTAGAGTGTGTGCAACAGCT 1143
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Db 1654 GATTTACAGTGCATTCTGAAGAGAGAGACATCAACAGAAATAGAGATTGCGAACAGCT 1713  
Qy 1144 CTTTTGAGAGAGGCTTAAAGACAGAGAGAAAGGTCTTCAATCGTGGAAGAAATPAA 1203  
Db 1714 CTTTTGAGAGAGGCTTAAAGACAGAGAGAAAGGTCTTCAATCGTGGAAGAAATPAA 1773  
Qy 1204 ATGTTGTATTAAATAGATACACAGCTAGTTCAGAGTTACCATGTATCCACTAGC 1263  
Db 1774 ATGTTGTATTAAATAGATACACAGCTAGTTCAGAGTTACCATGTATCCACTAGC 1833  
Qy 1264 TGGGTTCTGATTTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTCACTACAGGAAAAAA 1323  
Db 1834 TGGGTTCTGATTTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTCACTACAGGAAAAAA 1893  
Qy 1324 CTGTGCAAGTAGACACCTGATTCGGTTGCTTGTCTTAATCTAAAGCTCCATGCTCGG 1383  
Db 1894 CTGTGCAAGTAGACACCTGATTCGGTTGCTTGTCTTAATCTAAAGCTCCATGCTCGG 1953  
Qy 1384 CTTAAATCGTATAAACTCTGATATTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGAA 1443  
Db 1954 CTTAAATCGTATAAACTCTGATATTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGAA 2013  
Qy 1444 ACCAGAACATTTATGTACTACAAACCTGTTTTTAAAGAACTATGTTGCTATGAAT 1503  
Db 2014 ACCAGAACATTTATGTACTACAAACCTGTTTTTAAAGAACTATGTTGCTATGAAT 2073  
Qy 1504 TAAACTGTGCTGCTGATAGACAGACTGGA 1536  
Db 2074 TAAACTGTGCTGCTGATAGACAGACTGGA 2106

RESULT 5  
US-60-507-511-2084  
; Sequence 2084, Application US/60507511  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: AM 101081  
; CURRENT APPLICATION NUMBER: US/60/507,511  
; CURRENT FILING DATE: 2003-10-02  
; NUMBER OF SEQ ID NOS: 203623  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2084  
; LENGTH: 3007  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-507-511-2084

Query Match 99.7%; Score 1531; DB 7; Length 3007;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1531; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GTAAATTCAGTTTCCAGCAACAGGAACAGAGTACAGATCCTCAGCATGAGA 63  
Db 574 GTAAATTCAGTTTCCAGCAACAGGAACAGAGTACAGATCCTCAGCATGAGA 633  
Qy 64 GAATTTACTGTGCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCATCTATC 123  
Db 634 GAATTTACTGTGCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCATCTATC 693  
Qy 124 CAAGAAATAGGCTTGGTATGAGATTAGTACAGTAGAGGAAATGTATGATACAC 183  
Db 694 CAAGAAATAGGCTTGGTATGAGATTAGTACAGTAGAGGAAATGTATGATACAC 753  
Qy 184 TTACGTTTGTATGAAGATTGGGCTTGAAGACCCAGAGTACATATGCAAGTATGAT 243  
Db 754 TTACGTTTGTATGAAGATTGGGCTTGAAGACCCAGAGTACATATGCAAGTATGAT 813  
Qy 244 TTGTAGAAGTTAGGAACCCAGTATGGAACCTATATTAGGCGCTGGTGTCTCGTA 303

Db 814 TTGTAGAAGTTGAGBACCAGTGATGTAATATTAGGGCGCTGCTGTGGTTCTCGTA 873  
Qy 304 CTGTACACAGAAAAACAGATTTCTAAAGGAAATCAAAATTAGTAAGATTTGTATCTGATG 363  
Db 874 CTGTACACAGAAAAACAGATTTCTAAAGGAAATCAAAATTAGTAAGATTTGTATCTGATG 933  
Qy 364 AATATTTTCTCTTGAACACAGGGTCTGTCATCCACTACAACTATGTATGTCACCAATTC 423  
Db 934 AATATTTTCTCTTGAACACAGGGTCTGTCATCCACTACAACTATGTATGTCACCAATTC 993  
Qy 424 CAGAAGCTGTGAGTCTTCACTGCTACCCCTTCACTGCTTGGCCACTGGAACCTGTTAATA 483  
Db 994 CAGAAGCTGTGAGTCTTCACTGCTACCCCTTCACTGCTTGGCCACTGGAACCTGTTAATA 1053  
Qy 484 ATGCTATACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACACAGAGAT 543  
Db 1054 ATGCTATACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACACAGAGAT 1113  
Qy 544 GGCAAGTTGGACTTAGAAGATCTATATAGGCAACTTTGGCAACTTTCTTGGCAAGCTTTTG 603  
Db 1114 GGCAAGTTGGACTTAGAAGATCTATATAGGCAACTTTGGCAACTTTCTTGGCAAGCTTTTG 1173  
Qy 604 TTTTGGAGAAAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGAGGTAGATAT 663  
Db 1174 TTTTGGAGAAAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGAGGTAGATAT 1233  
Qy 664 ACAGCTCACACCTCTGTAACCTTCTCAGTGTCCATAAGGGAAGAACTAAAGAAACCGATA 723  
Db 1234 ACAGCTCACACCTCTGTAACCTTCTCAGTGTCCATAAGGGAAGAACTAAAGAAACCGATA 1293  
Qy 724 CCATTTTCTGCGCCAGGTTGCTCTCTGTTTAAACGCTGTGTGGAACTGTGCTCTGTTGTC 783  
Db 1294 CCATTTTCTGCGCCAGGTTGCTCTCTGTTTAAACGCTGTGTGGAACTGTGCTCTGTTGTC 1353  
Qy 784 TCCCAATTTGCAATGAATGTCAATGTCTCCACAGCAAGTTCTAATAAATAACACACAGG 843  
Db 1354 TCCCAATTTGCAATGAATGTCAATGTCTCCACAGCAAGTTCTAATAAATAACACACAGG 1413  
Qy 844 TCCTTTCAGTTGAGACCAAAACACCGGTCTCAGGGGATTCACAAATCACTCACGACGTGG 903  
Db 1414 TCCTTTCAGTTGAGACCAAAACACCGGTCTCAGGGGATTCACAAATCACTCACGACGTGG 1473  
Qy 904 CCCTGGAGCAACATGAGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGTAGCCGC 963  
Db 1474 CCCTGGAGCAACATGAGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGTAGCCGC 1533  
Qy 964 ATCACCAACAGCAGCTCTTGCCACAGAGCTGTGCAAGTGCAGTGGCTGATTTCTATTAGAAA 1023  
Db 1534 ATCACCAACAGCAGCTCTTGCCACAGAGCTGTGCAAGTGCAGTGGCTGATTTCTATTAGAAA 1593  
Qy 1024 CGTATGCTTATCTCCATCTTAACTCAGTTGTTGCTTCAAGGACCTTTTCATCTTTCAG 1083  
Db 1594 CGTATGCTTATCTCCATCTTAACTCAGTTGTTGCTTCAAGGACCTTTTCATCTTTCAG 1653  
Qy 1084 GATTTACAGTGCATTTCTGAAGAGGAGACATCAAAAGAAATTAGGAGTCTGCAACAGCT 1143  
Db 1654 GATTTACAGTGCATTTCTGAAGAGGAGACATCAAAAGAAATTAGGAGTCTGCAACAGCT 1713  
Qy 1144 CTTTTGAGAGAGGCTTAAAGGACAGGAAAAAGGTCTTCAATCGTGGAAGAAATPAA 1203  
Db 1714 CTTTTGAGAGAGGCTTAAAGGACAGGAAAAAGGTCTTCAATCGTGGAAGAAATPAA 1773  
Qy 1204 ATGTTGTATTAAATAGATACACAGCTAGTTCAGAGTTACCATGTATGTTCACTAGC 1263  
Db 1774 ATGTTGTATTAAATAGATACACAGCTAGTTCAGAGTTACCATGTATGTTCACTAGC 1833  
Qy 1264 TGGGTTCTGATTTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTCACTACAGGAAAAAA 1323  
Db 1834 TGGGTTCTGATTTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTCACTACAGGAAAAAA 1893  
Qy 1324 CTGTAGAAGTTAGGAACCCAGTATGGAACCTATATTAGGCGCTGGTGTCTCGTA 1383  
Db 1894 CTGTAGAAGTTAGGAACCCAGTATGGAACCTATATTAGGCGCTGGTGTCTCGTA 1953



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QY 1384 CCTAAATCGTATATAAATCTGGATTTTCTTTTCTTCTCATATTCACATATGTAA 1443
Db 1954 CCTAAATCGTATATAAATCTGGATTTTCTTTTCTTCTCATATTCACATATGTAA 2013
QY 1444 ACCGAAATCTATGTACTACAAACCTGGTTTAAAGGAACTATGTGTCTATGAAT 1503
Db 2014 ACCGAAATCTATGTACTACAAACCTGGTTTAAAGGAACTATGTGTCTATGAAT 2073
QY 1504 TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536
Db 2074 TAAACTTGTGTCGCTGATAGGACAGACTGGA 2106

RESULT 6
US-09-830-320A-8
; Sequence 8, Application US/09830320A
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AU-YOUNG, Janice K.
; TITLE OF INVENTION: GROWTH FACTOR RELATED MOLECULES
; FILE REFERENCE: PF-0627 USN
; CURRENT APPLICATION NUMBER: US/09/830,320A
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: PCT/US99/25458
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 60/183,024
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 60/155,216
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/172,233
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 8
; LENGTH: 2779
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No.: 4163378CB1
US-09-830-320A-8

Query Match 99.6%; Score 1529.4; DB 5; Length 2779;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1530; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTAATTCAGTTTCCAGCAACAAAGGACAGAACGGAGTACAGATCCTCAGCATGAGA 63
Db 340 GTAATTCAGTTTCCAGCAACAAAGGACAGTACGGAGTACAGATCCTCAGCATGAGA 399
QY 64 GAAATTTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATACTATTC 123
Db 400 GAAATTTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATACTATTC 459
QY 124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAAC 183
Db 460 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAAC 519
QY 184 TTACGTTTGAAGAAAGATTGGGCTTGAAGACCCAGAGAGATGACATATGCAAGTATGATT 243
Db 520 TTACGTTTGAAGAAAGATTGGGCTTGAAGACCCAGAGAGATGACATATGCAAGTATGATT 579
QY 244 TTGTAGAAGTTGAGGAACCCAGTATGGAACCTATATATTAGGCGCTGGTGTCTGTGTA 303
Db 580 TTGTAGAAGTTGAGGAACCCAGTATGGAACCTATATATTAGGCGCTGGTGTCTGTGTA 639
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QY 304 CTGTACAGGAAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTTGTATCTGATG 363
Db 640 CTGTACAGGAAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTTGTATCTGATG 699
QY 364 AATATTTTCTTCTCTGAACCAAGGTTCTGCATCCACTTACAAACATTTGTCTATGCCACAAATTC 423
Db 700 AATATTTTCTTCTCTGAACCAAGGTTCTGCATCCACTTACAAACATTTGTCTATGCCACAAATTC 759
QY 424 CAGAAGCTGTGAGTCCCTTCACTGTCTACCCCTTCACTTGTGCACTTGTGACCTGTCTTAATA 483
Db 760 CAGAAGCTGTGAGTCCCTTCACTGTCTACCCCTTCACTTGTGCACTTGTGACCTGTCTTAATA 819
QY 484 ATGCTATAACTGCTTTAGTACCTTGTGGAAGACCTTATTCGATATCTTTGAACCAAGAGAT 543
Db 820 ATGCTATAACTGCTTTAGTACCTTGTGGAAGACCTTATTCGATATCTTTGAACCAAGAGAT 879
QY 544 GGCAGTTTGGACTTTAGAAGATCTATATAGGCCAACTTTGGCAACTTTTGGCAAGGCTTTTG 603
Db 880 GGCAGTTTGGACTTTAGAAGATCTATATAGGCCAACTTTGGCAACTTTTGGCAAGGCTTTTG 939
QY 604 TTTTGGAGAGAAAATCCAGAGTGGTGGATCTGAACTTCTTAAACAGAGGAGGTAAAGATTAT 663
Db 940 TTTTGGAGAGAAAATCCAGAGTGGTGGATCTGAACTTCTTAAACAGAGGAGGTAAAGATTAT 999
QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTTAAAGAGAACCCGATA 723
Db 1000 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTTAAAGAGAACCCGATA 1059
QY 724 CCAATTTCTGGCCAGAGTTGTCTCTCGTTTAAACGCTGTGGTGGAACTGTGCTCTGTGTTC 783
Db 1060 CCAATTTCTGGCCAGAGTTGTCTCTCGTTTAAACGCTGTGGTGGAACTGTGCTCTGTGTTC 1119
QY 784 TCCACAATTTGCAATGAATGTCATGTCCTCAAGCAAGTTTACTAAAAAATACCCAGAGG 843
Db 1120 TCCACAATTTGCAATGAATGTCATGTCCTCAAGCAAGTTTACTAAAAAATACCCAGAGG 1179
QY 844 TCCTTCAGTTGAGACCAAAACACCGGTGTGAGGGGATTTGACAAATCACTCACCGACGTGG 903
Db 1180 TCCTTCAGTTGAGACCAAAACACCGGTGTGAGGGGATTTGACAAATCACTCACCGACGTGG 1239
QY 904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGGAGCACAGAGGATACCCGC 963
Db 1240 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGGAGCACAGAGGATACCCGC 1299
QY 964 ATCACCAACAGCAGCTCTTGTCCCAAGCTGTGCAAGTGTGCTGATTTCTATTAGAGAA 1023
Db 1300 ATCACCAACAGCAGCTCTTGTCCCAAGCTGTGCAAGTGTGCTGATTTCTATTAGAGAA 1359
QY 1024 CGTATGCGTTATCTCCATCTTAACTCTAGTGTGTTTGTCTTCAAGGACCTTTTCACTTCAG 1083
Db 1360 CGTATGCGTTATCTCCATCTTAACTCTAGTGTGTTTGTCTTCAAGGACCTTTTCACTTCAG 1419
QY 1084 GATTTACAGTGCATCTCTGAAGAGGAGACATCAAAACAGAAATTTAGGAGTTGTGCAACAGCT 1143
Db 1420 GATTTACAGTGCATCTCTGAAGAGGAGACATCAAAACAGAAATTTAGGAGTTGTGCAACAGCT 1479
QY 1144 CTTTGGAGAGGAGGCTTAAAGGACAGAGAAAGGCTTCTCAATCTGTGGGAAAAGAAATTTAA 1203
Db 1480 CTTTGGAGAGGAGGCTTAAAGGACAGAGAAAGGCTTCTCAATCTGTGGGAAAAGAAATTTAA 1539
QY 1204 ATGTTGTATTTAAATAGATCACAGCTAGTTTTCAGAGTTTACCATGTATTCCTACCTAGC 1263
Db 1540 ATGTTGTATTTAAATAGATCACAGCTAGTTTTCAGAGTTTACCATGTATTCCTACCTAGC 1599
QY 1264 TGGGTTCTGTATTTTCAAGTTCTTTTCGATACGGCTTTAGGGTAATGTCTAGTACAGGAAAAAA 1323
Db 1600 TGGGTTCTGTATTTTCAAGTTCTTTTCGATACGGCTTTAGGGTAATGTCTAGTACAGGAAAAAA 1659
QY 1324 CTGTGCAAGTACGACCTGATTCCTGCTTGTCTTAACTCTTAAAGCTCAATGTCTCTGGG 1383
Db 1660 CTGTGCAAGTACGACCTGATTCCTGCTTGTCTTAACTCTTAAAGCTCAATGTCTCTGGG 1719
QY 1384 CCTAAAAATCGTATFAAAATCTGGATTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAA 1443
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[illegible]

## RESULT 8

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US-09-876-813-32
/ Sequence 32, Application US/09876813
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Teresa
/ APPLICANT: Hart, Charles B.
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
/ FILE REFERENCE: 99-19
/ CURRENT APPLICATION NUMBER: US/09/876,813
/ CURRENT FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: US/09/564,595
/ PRIOR FILING DATE: 2000-05-03
/ PRIOR APPLICATION NUMBER: US 09/304,216
/ PRIOR FILING DATE: 1999-05-03
/ PRIOR APPLICATION NUMBER: US 60/164,463
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: US 60/180,169
/ PRIOR FILING DATE: 2000-02-04
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 32
/ LENGTH: 1760
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (154)...(1191)
US-09-876-813-32

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Query Match 98.4%; Score 1511; DB 5; Length 1760;  
Best Local Similarity 99.8%; Pred. NO. 0;  
Matches 1522; Conservative 1; Mismatches 1; Indels 1

4	QY	GTAAATTCAGTTTTCCAGCAACAGGACACAGACGAGTACAAGATCCTCCAGCATGAGA	63
236	Db	GTAAATTCAGTTTTCCAGCAACAGGACACAGGAGTACAAGATCCTCCAGCATGAGA	295
64	QY	GAATATTACTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATCTATTC	123
296	Db	GAATATTACTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATCTATTC	355
124	QY	CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAC	183
356	Db	CAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAC	415
184	QY	TTACGTTTCATGAAGAATTTGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATGATT	243
416	Db	TTACGTTTCATGAAGAATTTGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATGATT	475
244	QY	TTGTAGAAGTTGAGGAAACCCAGTGTATGAACTATATTAGGGCGCTGGTGTGGTTCGGTA	303
476	Db	TTGTAGAAGTTGAGGAAACCCAGTGTATGAACTATATTAGGGCGCTGGTGTGGTTCGGTA	535
304	QY	CTGTACAGGAAAAACAGATTTCTAAAGGAATCAAAATTAGGATPAAGATTTGTATCTGATG	363
536	Db	CTGTACAGGAAAAACAGATTTCTAAAGGAATCAAAATTAGGATPAAGATTTGTATCTGATG	595
364	QY	AATATTTTCTCTCTGAACAGAGGTTCTGCATCTCACTACAACTTGTCATGCCACAATTCA	423
596	Db	AATATTTTCTCTCTGAACAGAGGTTCTGCATCTCACTACAACTTGTCATGCCACAATTCA	655
424	QY	CAGAACTGTGAGTCCCTTCAGTGTACACCCCTTCAGCTTTGCCATCTGGACCTGCTTAATA	483
656	Db	CAGAACTGTGAGTCCCTTCAGTGTACACCCCTTCAGCTTTGCCATCTGCTTAATA	715
484	QY	ATGCTATAACTGCTTTAGTACTCTGGGAAGACCTTATTTCGATATCTCTTGAACACGAGAGAT	543
716	Db	ATGCTATAACTGCTTTAGTACTCTGGGAAGACCTTATTTCGATATCTCTTGAACACGAGAGAT	775
544	QY	GGCAGTTGGACTTAGAAGATCTATATAGGCAACTTTGGCAACTTCTTGGCAGGCTTTTGG	603

Db	776	GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAA	CTTCTTGGCAAGGCTTTTG	835
Qy	604	TTTTTGGAGAAATCCAGAGTGGTGATCTGAACCTTCTAA	CAGAGGAGGTAAAGATTAT	663
Db	836	TTTTTGGAGAAATCCAGAGTGGTGATCTGAACCTTCTAA	CAGAGGAGGTAAAGATTAT	895
Qy	664	ACAGCTGCACACTCGTAATCTCAGTGTCCATAGGGAAGAA	CTTAAAGAGAACCGATA	723
Db	896	ACAGCTGCACACTCGTAATCTCAGTGTCCATAGGGAAGAA	CTTAAAGAGAACCGATA	955
Qy	724	CCATTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGGT	TGGGAACCTGTGCTGTGTTC	783
Db	956	CCATTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGGT	TGGGAACCTGTGCTGTGTTC	1015
Qy	784	TCCACAAATTCGAATGAATGTCCAATGTCTCCAAAGCAAA	GTATTCTAAAAAATACCCAGAG	843
Db	1016	TCCACAAATTCGAATGAATGTCCAATGTCTCCAAAGCAAA	GTATTCTAAAAAATACCCAGAG	1075
Qy	844	TCCTTCAGTTGAGACAAASACCGTGTGAGGGATTGCACAA	TACTCACCGACGTGG	903
Db	1076	TCCTTCAGTTGAGACAAASACCGTGTGAGGGATTGCACAA	TACTCACCGACGTGG	1135
Qy	904	CCCTGGAGCACCATGAGGAGTGTACTGTGTGTCAGAGGGAG	CACACAGAGGATACCCG	963
Db	1136	CCCTGGAGCACCATGAGGAGTGTACTGTGTGTCAGAGGGAG	CACACAGGAGTATGCCG	1195
Qy	964	ATCACCACACGACGCTCTTGCCCGAGAGCTGTGCAGTGC	AGTGGCTGATTTATGAGAA	1023
Db	1196	ATCACCACACGACGCTCTTGCCCGAGAGCTGTGCAGTGC	AGTGGCTGATTTATGAGAA	1255
Qy	1024	CGTATCGGTATCTCCATCCTTAATCTCAGTTCTTTGCTT	CAAGGACCTTTCACTTTTCA	1083
Db	1256	CGTATCGGTATCTCCATCCTTAATCTCAGTTCTTTGCTT	CAAGGACCTTTCACTTTTCA	1315
Qy	1084	GATTTACAGTGCATTTCTGAAAGAGGAGACATCAAA	CAGAATTAGGAGTTGTGCAACAGCT	1143
Db	1316	GATTTACAGTGCATTTCTGAAAGAGGAGACATCAAA	CAGAATTAGGAGTTGTGCAACAGCT	1375
Qy	1144	CTTTTGAGAGGAGCCCTAAAGGACAGGAGAAAGGCTCTT	CAATCGTGGAAAGAAATTAA	1203
Db	1376	CTTTTGAGAGGAGCCCTAAAGGACAGGAGAAAGGCTCTT	CAATCGTGGAAAGAAATTAA	1435
Qy	1204	ATGTTGTATTAAATAGATCACACGCTAGTTTTCAGAGTT	TACCATGTACGTTATCCACTAGC	1263
Db	1436	ATGTTGTATTAAATAGATCACACGCTAGTTTTCAGAGTT	TACCATGTACGTTATCCACTAGC	1495
Qy	1264	TGGTTCCTGTATTTTCAGTTCTTTTCGATACGGCTTAT	GAGTAACTGCAGTACAGAAATAA	1323
Db	1496	TGGTTCCTGTATTTTCAGTTCTTTTCGATACGGCTTAT	GAGTAACTGCAGTACAGAAATAA	1555
Qy	1324	CTGTGCAAGTGAGCACCTCGATTCGGTTGCCCTTGCTT	AACTCTAAAGCTCCATGTCCTGGG	1383
Db	1556	CTGTGCAAGTGAGCACCTCGATTCGGTTGCCCTTGCTT	AACTCTAAAGCTCCATGTCCTGGG	1615
Qy	1384	CCTAAATCGTATAAAATCTGGA-TTTTTTTTTTTTTTTT	TTTTTGTCTCATATTTTCATATGTA	1442
Db	1616	CCTAAATCGTATAAAATCTGGA-TTTTTTTTTTTTTTTT	TTTTTGTCTCATATTTTCATATGTA	1675
Qy	1443	AACACAGAACATCTTATGTACTACAAACCTGGTTTTT	AAAAAGGAACTATGTCGTATGAA	1502
Db	1676	AACACAGAACATCTTATGTACTACAAACCTGGTTTTT	AAAAAGGAACTATGTCGTATGAA	1735
Qy	1503	TTAAACTTGTGTCATGCTGATAGGA	1527	
Db	1736	TTAAACTTGTGCTGCTGATAGGA	1760	

RESULT 9  
US-10-664-432-1  
; Sequence 1, Application US/10664432  
; GENERAL INFORMATION:  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Gilbertson, Debra G.

```

; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/10/664,432
; CURRENT FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
; US-10-664-432-1

Query Match      98.4%; Score 1511; DB 6; Length 1760;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1522; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      4 GTAAATTCAGTTTCCAGCAACRAGGACAGAACGGAGTACAGATCCTCAGCATGAGA 63
DB      236 GTAAATTCAGTTTCCAGCAACRAGGACAGAACGGAGTACAGATCCTCAGCATGAGA 295
QY      64 GAATTTATTACTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCATCTTATC 123
DB      296 GAATTTATTACTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCATCTTATC 355
QY      124 CAAGAAATACGCTCTTGTGATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAC 183
DB      356 CAAGAAATACGCTCTTGTGATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAC 415
QY      184 TTACGTTTGTATCAAAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
DB      416 TTACGTTTGTATCAAAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 475
QY      244 TTGTAGAAAGTTGAGGAACCCAGTAGTATGAACTATATATGAGGCGCTGTGTGTTCTGTA 303
DB      476 TTGTAGAAAGTTGAGGAACCCAGTAGTATGAACTATATATGAGGCGCTGTGTGTTCTGTA 535
QY      304 CTGTACCCAGGAAACAGATTTCTAAGGAAATCAAAATAGGATAGATTGTATCTGATG 363
DB      536 CTGTACCCAGGAAACAGATTTCTAAGGAAATCAAAATAGGATAGATTGTATCTGATG 595
QY      364 AATATTTCTCTTGAAACAGGGTCTGCATCCATACAACTATGTCATGCAACAAATCA 423
DB      596 AATATTTCTCTTGAAACAGGGTCTGCATCCATACAACTATGTCATGCAACAAATCA 655
QY      424 CAGAGCTGTGACTCCTTCAGTGTCTACCCCTTCCAGTTTGCCTTGCCTGCTTAATA 483
DB      656 CAGAGCTGTGACTCCTTCAGTGTCTACCCCTTCCAGTTTGCCTTGCCTGCTTAATA 715
QY      484 ATGCTATAACTGCTCTTAGTACTTGGAGACCTTATTCGATATCTTGAACACAGAGAT 543
DB      716 ATGCTATAACTGCTCTTAGTACTTGGAGACCTTATTCGATATCTTGAACACAGAGAT 775
QY      544 GGCAGTTGCACTTAGAGATCTATATAGCCCACTTGGCACTTCTTGGCAGGCTTTTG 603
DB      776 GGCAGTTGCACTTAGAGATCTATATAGCCCACTTGGCACTTCTTGGCAGGCTTTTG 835
QY      604 TTTTTCGAGAAATCCAGAGTGGTGGATCTGAACCTTCTTAACAGAGGAGGTAAGATTAT 663
DB      836 TTTTTCGAGAAATCCAGAGTGGTGGATCTGAACCTTCTTAACAGAGGAGGTAAGATTAT 895
QY      664 ACAGCTGCACCTCTGTAATCTTCTAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 723
DB      896 ACAGCTGCACCTCTGTAATCTTCTAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 955
QY      724 CCATTTTCTGGCCAGGTGTCTCTGTTAAAGCTGTGTGGAACTGTGCTGTCTGTC 783
DB      956 CCATTTTCTGGCCAGGTGTCTCTGTTAAAGCTGTGTGGAACTGTGCTGTCTGTC 1015
QY      784 TCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCAGAGG 843

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DB      1016 TCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCAGAGG 1075
QY      844 TCCTTCAGTTGAGACCAAAASACCGGTGTGAGGGGATTGACAAATCACTCCAGCGTGG 903
DB      1076 TCCTTCAGTTGAGACCAAAASACCGGTGTGAGGGGATTGACAAATCACTCCAGCGTGG 1135
QY      904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGAGGAGGAGCAGAGGAGATACCGC 963
DB      1136 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGAGGAGGAGCAGAGGAGATACCGC 1195
QY      964 ATCAACCAACAGCAGCTCTTCCAGAGCTGTGCAAGTGTGCAAGTGTGCTGATTTCTATAGAGAA 1023
DB      1196 ATCAACCAACAGCAGCTCTTCCAGAGCTGTGCAAGTGTGCAAGTGTGCTGATTTCTATAGAGAA 1255
QY      1024 CGTATGCGTTATCTCCATCCTTAATCTCAGTTGTGTTTGTCTTCAAGGACCTTTCTATCTTCAG 1083
DB      1256 CGTATGCGTTATCTCCATCCTTAATCTCAGTTGTGTTTGTCTTCAAGGACCTTTCTATCTTCAG 1315
QY      1084 GATTTACAGTGCATCTCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCT 1143
DB      1316 GATTTACAGTGCATCTCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCT 1375
QY      1144 CTTTTCAGAGAGGAGGCTTAAAGGACAGAGAAAGGCTTCTCAATTCGTGGAAGAAATTA 1203
DB      1376 CTTTTCAGAGAGGAGGCTTAAAGGACAGAGAAAGGCTTCTCAATTCGTGGAAGAAATTA 1435
QY      1204 ATGTTGTATTAATAGATACACAGCTAGTTTTCAGAGTTACCATGTAGTATTCACCTAGC 1263
DB      1436 ATGTTGTATTAATAGATACACAGCTAGTTTTCAGAGTTACCATGTAGTATTCACCTAGC 1495
QY      1264 TGGTCTCTGATTTTCAAGTCTTTCGATAACGCTTTCAGAGTAAATGTCAAGTACAGGAAAAA 1323
DB      1496 TGGTCTCTGATTTTCAAGTCTTTCGATAACGCTTTCAGAGTAAATGTCAAGTACAGGAAAAA 1555
QY      1324 CTGTGCAAGTACAGCAGCTGATTCGTTGCTTAACTCTAAAGCTCCATGTCTCTGGG 1383
DB      1556 CTGTGCAAGTACAGCAGCTGATTCGTTGCTTAACTCTAAAGCTCCATGTCTCTGGG 1615
QY      1384 CCTAAAACTGTATAAAAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTGTCTCATATATGTA 1442
DB      1616 CCTAAAACTGTATAAAAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTGTCTCATATATGTA 1675
QY      1443 AACAGAACATTCATGTACTACAACTGTTTAAAAAGGAACTATGTGCTATGAA 1502
DB      1676 AACAGAACATTCATGTACTACAACTGTTTAAAAAGGAACTATGTGCTATGAA 1735
QY      1503 TTAACCTTGTCTCATGCTGATAGGA 1527
DB      1736 TTAACCTTGTCTCATGCTGATAGGA 1760

```

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RESULT 10
US-09-457-066-50
; Sequence 50, Application US/09457066
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Artificial Sequence

```



QY 664 ACAGTGCACACCTCTGTAATCTCTCAAGTGTCCATTAAGGAGAGAACTAAGAGAACCGATA 723  
 DB 1791 ACAGTGCACACCCCGAACTTCTCAGTGTCCATACCGGAGAGCTTAAAGAGGACAGATA 1850  
 QY 724 CCATTTCTGGCCAGGTGTCTCCTGTTAAACGCTGTGTGGAACTGTGCTGTGTTC 783  
 DB 1851 CCATTTCTGGCCAGGTGTCTCCTGTTAAACGCTGTGTGGAACTGTGCTGTGTTC 1910  
 QY 784 TCACAAATTGCAATGAATGTCAATGTGTCCCAAGCAAGTTCATAAAAAATACCAAGG 843  
 DB 1911 TCACAAATTGCAATGAATGTCAATGTGTCCCAAGCAAGTTCATAAAAAATACCAAGG 1970  
 QY 844 TCCTTCAGTTGAGACCAAAACCGGTGTCAAGGGATTGACAAATCACTCACCGAGCTG 903  
 DB 1971 TCCTTCAGTTGAGACCAAAACCGGTGTCAAGGGATTGACAAATCACTCACCGAGCTG 2030  
 QY 904 CCCTGGAGCACCATTGAGAGTGTGACTGTGTGTCGAGAGGAGCACAGAGGATACCCGC 963  
 DB 2031 CTCTGGAACACACGAGGATGTGACTGTGTGTGAGAGGAAACCGAGAGGTAACCTGC 2090  
 QY 964 ATCACCACAGCAGCTC 980  
 DB 2091 AGCCTTCGTAGCAGCAC 2107

## RESULT 12

US-09-876-813-34  
 ; Sequence 34, Application US/09876813  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gilbert, Teresa  
 ; APPLICANT: Hart, Charles E.  
 ; APPLICANT: Sheppard, Paul O.  
 ; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
 ; FILE REFERENCE: 99-19  
 ; CURRENT APPLICATION NUMBER: US/09/876,813  
 ; CURRENT FILING DATE: 2001-06-06  
 ; PRIOR APPLICATION NUMBER: US/09/564,595  
 ; PRIOR FILING DATE: 2000-05-03  
 ; PRIOR APPLICATION NUMBER: US 09/304,216  
 ; PRIOR FILING DATE: 1999-05-03  
 ; PRIOR APPLICATION NUMBER: US 60/164,463  
 ; PRIOR FILING DATE: 1999-11-10  
 ; PRIOR APPLICATION NUMBER: US 60/180,169  
 ; PRIOR FILING DATE: 2000-02-04  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 34  
 ; LENGTH: 3571  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1049) ... (2086)  
 ; US-09-876-813-34

Query Match 46.9%; Score 721; DB 5; Length 3571;

Best Local Similarity 83.6%; Pred. No. 4.1e-218;  
 Matches 817; Conservative 0; Mismatches 160; Indels 0; Gaps 0;  
 QY 4 GTAAATTCAGTTTCCAGCAACAAAGGACAGAGACGAGTACAGATCTCCAGCATGAGA 63  
 DB 1131 GCAAGTTGCAGCTCTCCAGCAGCAGGACAGAGACGAGTCCAGATCCCGGATGAGA 1190  
 QY 64 GAAATTTACTGTGTCTACTAATGAAGATTTCAAGCCCAAGTTTCTCCTCATCTATTC 123  
 DB 1191 GAGTTGTCACTATATCTGGTAATGGAGCATCCACAGCCGAAAGTTTCTCATACATACC 1250  
 QY 124 CAAGAAATACGCTCTTGTGTAGGAGATTAGTAGCAGTAGAGGAAATGTGATGATCAAC 183  
 DB 1251 CAAGAAATATGCTGTGTGTGGAGATTAGTTGAGTAGATGAAATGTGCGGATCAGC 1310  
 QY 184 TTACGTTTGTGAAGAATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243

DB 1311 TCACATTTGATGAGAGATTTGGGCTGGAAGATCCAGAAGACGATATATGCAAGTATGATT 1370  
 QY 244 TTGTAGAAGTTGAGAAACCCAGTGTATATGGAACATATATAGGCGGTGTGTGTGTTGCTGA 303  
 DB 1371 TTGTAGAAGTTGAGAGAGCCAGTGTATGGAAGTGTGTTTAGGACGCTGTGTGTGTTGCTGA 1430  
 QY 304 CTGTACACAGGAAACACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTGTTATCTGATG 363  
 DB 1431 CTGTGCCAGGAAAGCAGAGATTCTAAAGGAATCATATCAGGATAAGATTGTTATCTGATG 1490  
 QY 364 AATATTTCTTCTTGAAACCAAGGTTCTGCATCCACTCAACATTTGTCTCATGCGCAAAATTC 423  
 DB 1491 AGTATTTTCCATCTGAAACCCGGAATTCGCATCCACTCAAGTATATCATGTCACCAAGTCA 1550  
 QY 424 CAGAGCTGTGAGTCTTCACTGCTACCCCTTCCAGCTTTCCTGACCTGACCTGCTTAAATA 483  
 DB 1551 CAGAAACCAAGTCTTTCGGTGTTCGCCCTTTCATCTTTGTCTGTCAGCTGCTCAACA 1610  
 QY 484 ATGCTATTAACCTGCTTTAGTACCTTTGGAAGACCTTTATTCGATATCTTGAACCAAGAGAT 543  
 DB 1611 ATGCTGTGACTGCTTCACTGCTTTCGAGTACCTTGGAGAGCTGATTGCGGTACCTAGAGCCAGATCGAT 1670  
 QY 544 GGCAGTTGGAATTAGAAGATCTATATAGGCCAACTTGSCAACTTCTTGSCAAGGCTTTTG 603  
 DB 1671 GGCAGGTGGAATTGGAAGCTCTCAAGCCCAACATGCGAGCTTTTGGGCAAGGCTTTTCC 1730  
 QY 604 TTTTGGAAAGAAATCCAGAGTGGTGGATCTGAACCTTTCTAACAGAGGAGGTAAAGATTAT 663  
 DB 1731 TGTATGGGAAAGAAAGCAAGTGGTGAATCTGAATCTCTCTCAAGGAAGAGGTAAACCTCT 1790  
 QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTTAAAGAGAACCGATA 723  
 DB 1791 ACAGCTGCACACCCCGAACTTCTCAGTGTCCATAAGGGAAGAGCTTAAAGAGGACAGATA 1850  
 QY 724 CCATTTCTGGCCAGGTTGTCTCCTGTTAAACGCTGTGTGGAACTGTGCTGCTGTTC 783  
 DB 1851 CCATATTTCTGGCCAGGTTGTCTCCTGTTCAAGCGCTGTGGAGGAAATTTGCTGCTGTTC 1910  
 QY 784 TCCCAAAATTCGAATGAATGTCAATGTGTGCCCAAGCAAGTTTACTAAAAAATACCAAGG 843  
 DB 1911 TCCCAAAATTCGAATGAATGTCAATGTGTGCCCAAGCAAGTTTACTAAAAAATACCAAGG 1970  
 QY 844 TCCTTCAGTTGAGACCAAAACCGGTGTCCAGGGGATTCACAAATCACTCACCGAGCTGG 903  
 DB 1971 TCCTTCAGTTGAGACCAAAACCGGTGTCCAGGATTCGATTAAGTCACTCACTGATGTTG 2030  
 QY 904 CCCTGGAGCACCATTGAGAGTGTGACTGTGTGTCGAGAGGAGCACAGAGGATAGCCGC 963  
 DB 2031 CTCTGGAACACACGAGGATGTGACTGTGTGTGAGAGGAAACCGAGAGGTAACCTGC 2090  
 QY 964 ATCACCACAGCAGCTC 980  
 DB 2091 AGCCTTCGTAGCAGCAC 2107

## RESULT 13

US-10-664-432-3  
 ; Sequence 3, Application US/10664432  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gilbertson, Debra G.  
 ; APPLICANT: Hart, Charles E.  
 ; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
 ; TITLE OF INVENTION: LIGAMENT AND CARTILAGE  
 ; FILE REFERENCE: 00-12  
 ; CURRENT APPLICATION NUMBER: US/10/664,432  
 ; CURRENT FILING DATE: 2003-09-19  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 3571  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus

/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: (1049) ... (2086)  
US-10-664-432-3

Query Match 46.9%; Score 721; DB 6; Length 3571;  
Best Local Similarity 83.6%; Pred. No. 4.1e-218;  
Matches 817; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

```
QY 4 GTAAATTCAGTTTTCAGCAACAAAGGAAACAGACCGAGTACAAAGATCCTCAGCATGAGA 63
Db 1131 GCAAGTTGAGCTCTCCAGCGACAAGGAAACAGAACGAGTGCAGATCCCGGCATGAGA 1190
QY 64 GAATTATCTGCTCTCTAATGGAAGTATTCACAGCCCAAGTTTCCTCATCTATTC 123
Db 1191 GAGTTGTCTATATCTGTTAATGGAGCATCCACAGCCCGAAGTTTCCTCATACATCC 1250
QY 124 CAAGAATACGCTCTGGTATGAGATTTAGCAGTAGGAGAAATGTATGATACAC 193
Db 1251 CAAGAATATGGTCTGGTGTGAGATTTAGTGCAGTAGATGAATGTGCGATCCAGC 1310
QY 184 TTACGTTTGATGAAGATTTGGGCTTGAGACCCAGAGATGACATATGCAAGTATGATT 243
Db 1311 TGACATTTGATGAGATTTGGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATT 1370
QY 244 TTGTAGAGTTGAGGAACCCAGTGTGGAACATATATAGGGCGCTGGTGTCTGGTA 303
Db 1371 TTGTAGAGTTGAGGACCCAGTGTGGAAGTGTGTTAGGACGCTGGTGTCTGGGA 1430
QY 304 CTGTACAGGAAACAGATTTCTAAAGGAATCAAATTAGGATAAGATTTGTATCTGATG 363
Db 1431 CTGTGACAGGAAGAGAGATTTCTAAAGGAATCATATCAGATGAAGATTTGTATCTGATG 1490
QY 364 AATATTTCTCTGAAACCAAGGTTCTGCATCCACTACAAATGTCATGCCCAATTC 423
Db 1491 AGTATTTCTCATCTGAACCCGATTTCTGCATCCACTACAGTATATCATGSCCAAGTCA 1550
QY 424 CAGAAGCTGTGAGTCTCTCAGTCTACCCCTTCAGCTTTGACCTGGACCTGCTTAATA 483
Db 1551 CAGAAACCAAGTCTCTGGTGTGGCCCTTCATCTTTGTCAATGGACCTGCTCAACA 1610
QY 484 ATGCTATAACTGCTTTAGTACCTTGGAAAGACCTTATTCGATATCTTGAACACAGAGAT 543
Db 1611 ATGCTGTGACTGCTTCAGTACCTTGGAGAGCTGATTCGGTACCTAGAGCCAGATCGAT 1670
QY 544 GGCAGTTGACCTTAGAAGATCTATATAGGCCAATCTTGGCAACTCTTGGCAAGGCTTTTG 603
Db 1671 GGCAGTTGACCTTGGACAGCTCTACAAGCCACATGGCAGCTTTTGGCAAGGCTTTTC 1730
QY 604 TTTTGGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGTAAAGATTAT 663
Db 1731 TGTATGGGAAGAAAGCAAGTGGTGAATCTGAATCTCTCTCAAGGAAGAGGTAAAACTCT 1790
QY 664 ACAGCTGCACACTCGTAACTTCTCAGTGTCCATAGGGAAGAACTTAAAGAGAACCGATA 723
Db 1791 ACAGCTGCACACCCCGAACTTCTCAGTGTCCATAGCGGAAGCTTAAAGAGACAGATA 1850
QY 724 CCATTTCTGGCCAGGTTGCTCTGGTTAAAGCTGTGGTGGAACTCTGTGCTGTGTGC 783
Db 1851 CCATATTTGGCCAGGTTGCTCTGGTCAAGCGCTGTGGAGAAATTTGTGCTGTGTGC 1910
QY 784 TCCAAATTTGCAATGAATGCTCAATGTCTCCAGCAAGTTACTTAAAGAAATACCCAGAG 843
Db 1911 TCCATTAATTTGCAATGAATGCTCAATGTCTCCAGCTTAAAGTTACAAAAAGTACCATGAG 1970
QY 844 TCTTCAAGTTGAGACCAASACCGGTGTTCAGGGGATTTGCACAAATCACTCACCGAGTGG 903
Db 1971 TCTTCAAGTTGAGACCAASACCGGTGTTCAGGGGATTTGCATAGTCACTCACTGATGTGG 2030
QY 904 CCTGGAGCACCATGAGGAGTGTGCTGTGTGAGAGGGAGCAAGAGGATAGCCGC 963
Db 2031 CTCTGGAACACACGAGGAATGTGCTGTGTGTAGAGGAAACGAGGAGGTAACTGC 2090
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QY 964 ATCACCACCAGCAGCTC 980
Db 2091 AGCCTTCGTAGCAGCAC 2107
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RESULT 14

US-60-487-610-19346  
; Sequence 19346, Application US/60487610  
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele  
; APPLICANT: HUANG, Hongjin  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
; FILE OF INVENTION: METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001469  
; CURRENT APPLICATION NUMBER: US/60/487,610  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 97101  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19346  
; LENGTH: 221510  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(221510)  
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1  
US-60-487-610-19346

Query Match 45.2%; Score 694.4; DB 7; Length 221510;  
Best Local Similarity 97.8%; Pred. No. 1.1e-208;  
Matches 698; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

```
QY 823 TTAATAAAATATACACGAGGTCTTCAGTTGAGACCAACCGGTGTCAGGGATTGC 882
Db 213895 TTAATCTTATCCCTTTCAGTTCAGTTGAGACCAACCGGTGTCAGGGATTGC 213954
QY 883 ACAATATCACTACCCGAGTGGCCCTGGAGCACCATGAGAGTGTGACTGTGTGCAGAG 942
Db 213955 ACAATCACTACCCGAGTGGCCCTGGAGCACCATGAGAGTGTGACTGTGTGCAGAG 214014
QY 943 GGAGCACAGAGGATAGCGCATCAACACAGCAGCTCTTGGCCAGAGCTGTGCAGTCA 1002
Db 214015 GGAGCACAGGAGTAGCGCATCAACACAGCAGCTCTTGGCCAGAGCTGTGCAGTCA 214074
QY 1003 GTGGCTGATTCTATTAGAGAGCTATGCTTATCCATCTTAATCTCAGTTGTTGCT 1062
Db 214075 GTGGCTGATTCTATTAGAGACRTATGCGTTATCTCCATCTTAATCTCAGTTGTTGCT 214134
QY 1063 TCAAGGACCTTTTCATCTTCAGGATTTTACAGTGCATTTCTGAAAGAGAGACATCAAAACAGA 1122
Db 214135 TCAAGGACCTTTTCATCTTCAGGATTTTACAGTGCATTTCTGAAAGAGAGACATCAAAACAGA 214194
QY 1123 ATTAGAGTGTGCAACAGCTCTTTTGAGAGAGGCTTAAAGACAGGAGAAAAGTCTTT 1182
Db 214195 ATTAGAGTGTGCAACAGCTCTTTTGAGAGAGGCTTAAAGACAGGAGAAAAGTCTTT 214254
QY 1183 CAATCGTGAAGAAAATTAATGTTGATTAAATAGATCACCGCTAGTTTCAGAGTTA 1242
Db 214255 CAATCGTGAAGAAAATTAATGTTGATTAAATAGATCACCGCTAGTTTCAGAGTTA 214314
QY 1243 CCATGTAGCTATTCATCTAGCTGGGTTCGTATTTTCAGTTCTTTTCATACGGCTTAGGGT 1302
Db 214315 CCATGTAGCTATTCATCTAGCTGGGTTCGTATTTTCAGTTCTTTTCATACGGCTTAGGGT 214374
QY 1303 ATGTGAGTACAGGAAAAAACTGTGCAAGTGAAGCACTGATCCGTTCCTTGCCTTAAC 1362
Db 214375 ATGTGAGTACAGGAAAAAACTGTGCAAGTGAAGCACTGATCCGTTCCTTGCCTTAAC 214434
QY 1363 TCTAAAGCTCCATGTCTCGGGCTAAATCGTATAAATCTGATTTTTTTTTTTTTTTTTT 1422
Db 214435 TCTAAAGCTCCATGTCTCGGGCTAAATCGTATAAATCTGATTTTTTTTTTTTTTTTTT 214494
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QY 1423 TCGTCATATTACATATGTAACACGAGAACATTCTATGTACTACAAACCTGGTTTTTAAAA 1482
Db 214495 TCGTCATATTACATATGTAACACGAGAACATTCTATGTACTACAAACCTGGTTTTTAAAA 214554

QY 1483 AGGAACATGTGGCTATCAATTTAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536
Db 214555 AGGAACATGTGGCTATCAATTTAAACTTGTGTCATGCTGATAGGACAGACTGGA 214608

RESULT 15
US-60-485-450-11913
; Sequence 11913, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11913
; LENGTH: 221510
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(221510)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Ta
US-60-485-450-11913

```

Query Match	45.2%	Score 694.4	DB 7	Length 221510
Best Local Similarity	97.8%	Pred. No. 1.1e-208		
Matches 698	Conservative 5	Mismatches 11	Indels 0	Gaps 0
QY	823	TTACTAAAAATACACAGAGTCTTTAGTTTGAGACCAAAACCGTGTTCAGGGGATTGC	882	
Db	213895	TTACTCTTATTCCTTTTCAGTCTCTTTAGTTTGAGACCAAAACCGTGTTCAGGGGATTGC	213954	
QY	883	ACAAATCACTCACCGAAGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGCAGAG	942	
Db	213955	ACAAATCACTCACCGAAGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGCAGAG	214014	
QY	943	GGAGCACHGAGGAGTAGCCGCATACCAACAGCAGCCTCTTGCCACAGAGCTGTGCAGTGCA	1002	
Db	214015	GGAGCACHGAGGAGTAGCCGCATACCAACAGCAGCCTCTTGCCACAGAGCTGTGCAGTGCA	214074	
QY	1003	GTGCGTGATTCATTATAGAGAACGTATGCGTTATCTCCATCTTAAATCTCAGTTGTTGCT	1062	
Db	214075	GTGCGTGATTCATTATAGAGAACGTATGCGTTATCTCCATCTTAAATCTCAGTTGTTGCT	214134	
QY	1063	TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTTCTGAAGAGGAGACATCAACACAGA	1122	
Db	214135	TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTTCTGAAGAGGAGACATCAACACAGA	214194	
QY	1123	ATTAGAGTTGTGCACAGCTCTTTTGAGAGAGGCCCTAAAGGACAGAGAAAAGGCTTT	1182	
Db	214195	ATTAGAGTTGTGCACAGCTCTTTTGAGAGAGGCCCTAAAGGACAGAGAAAAGGCTTT	214254	
QY	1183	CAATCGTGGAAAGAAAATTAAGTTGTATTAATATAGATCACACGTAGTTTCAGAGTTA	1242	
Db	214255	CAATCGTGGAAAGAAAATTAAGTTGTATTAATATAGATCACACGTAGTTTCAGAGTTA	214314	
QY	1243	CCATGTAGCGTATTCACACTAGCTGGGTTCTGTATTTTCAGTTCTTTCCGATACGGCTTAGGGT	1302	
Db	214315	CCATGTAGCGTATTCACACTAGCTGGGTTCTGTATTTTCAGTTCTTTCCGATACGGCTTAGGGT	214374	
QY	1303	AATGTCAGTACAGGAAAAAAACTGTGCAAGTGAGGACACCTGATTCGGTGGCCCTTGCTTAAC	1362	
Db	214375	AATGTCAGTACAGGAAAAAAACTGTGCAAGTGAGGACACCTGATTCGGTGGCCCTTGCTTAAC	214434	

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OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 23:39:26 ; Search time 2241.28 Seconds  
(without alignments)  
16656.442 Million cell updates/sec

Title: US-09-852-209A-4

Perfect score: 1536

Sequence: 1 cgggtaattccagtttcc.....tgctgtaggacagactgga 1536

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hcc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_man:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_fod:\*  
26: em\_gss\_ptg:\*  
27: em\_gss\_vri:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1484.8	96.7	2826	11	BC041783
2	1481.4	96.4	2655	11	BC051876
3	787.2	51.3	999	13	BQ068266
4	779.6	50.8	969	10	BG677432

5	767.6	50.0	811	10	BG185961
6	758.8	49.4	1142	10	BG681390
7	733	47.7	802	12	BI870535
8	721	46.9	2765	11	AK052947
9	721	46.9	3244	11	AK033734
10	721	46.9	3405	11	AK042767
11	696.8	45.4	769	14	CB309471
12	693.8	45.2	2893	11	BC029099
13	640	41.7	686	12	BQ015321
14	604.2	39.3	2502	11	AK081347
15	572.4	37.3	789	12	BI911795
16	568	37.0	572	13	BQ694737
17	519.8	33.8	696	10	BG430400
18	489.4	31.9	567	12	BM827309
19	489.2	31.8	823	13	BU614825
20	489	31.8	500	10	BE326924
21	481.8	31.4	523	10	BE958470
22	481.4	31.3	982	13	BU459467
23	478.4	31.1	851	10	BF102859
24	478.2	31.1	950	10	BF031624
25	477.6	31.1	902	13	BU517879
26	473.8	30.8	820	10	BF697294
27	473	30.8	874	10	BF670092
28	466.4	30.4	676	13	BU259419
29	465.8	30.3	565	10	BE884591
30	456	29.7	695	12	BI668022
31	443.6	28.9	556	10	BG609411
32	432.2	28.1	877	10	BF137533
33	431	28.1	477	14	CB159806
34	411.4	26.8	559	12	BM053696
35	411	26.8	412	14	W21436
36	408	26.6	425	9	AA759138
37	407.8	26.5	564	10	BF151355
38	407.4	26.5	889	10	BF698737
39	401.4	26.1	983	10	BG112388
40	387	25.2	562	9	AU280428
41	386.8	25.2	764	10	BF541705
42	384.4	25.0	523	10	BF021679
43	378.8	24.7	511	9	AW210331
44	378.6	24.6	968	10	BG118707
45	374.6	24.4	618	10	BG221261

#### ALIGNMENTS

RESULT 1

BC041783

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

BC041783 2826 bp mRNA linear HTC 13-JAN-2003  
Homo sapiens, Similar to platelet-derived growth factor, C  
polypeptide, clone IMAGE:4614150, mRNA.

BC041783.1 GI:27692870

HTC.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 2826)

Strausberg, R.

Direct Submission

Submitted (23-DEC-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgabbs-f@mail.nih.gov](mailto:cgabbs-f@mail.nih.gov)

Tissue Procurement: CLONTECH

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305